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Run on: December 30, 2004, 16:04:46 ; Search time 37 Seconds

32.263 Million cell updates/sec

### OM protein - protein search, using SW model

Title: US-10-718-321-1  
Perfect score: 99  
Sequence: 1 SSDGLWNNTQOLFLEHS 18

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database : ISSUED PATENTS AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilesl.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	99	100.0	334	4	US-03-197-970B-7 Sequence 7, Appli
2	84.8	84.8	451	5	US-03-287-001A-2 Sequence 2, Appli
3	84	84.8	451	5	PCT-US95-09941-2 Sequence 2, Appli
4	52.5	52.5	570	4	US-03-248-796A-15079 Sequence 13, Appli
5	48.5	48.5	981	4	US-03-09-991-258-13 Sequence 13, Appli
6	45	45.5	114	6	5514582-13 Patent No. 5514582 Sequence 1, Appli
7	45	45.5	114	6	5514582-14 Sequence 1, Appli
8	45	45.5	1464	1	US-03-026-138B-1 Sequence 1, Appli
9	44	44.4	590	4	US-03-538-092-967 Sequence 1, Appli
10	43	43.4	62	4	US-03-248-796A-22793 Sequence 1, Appli
11	43	43.4	251	4	US-03-270-767-49147 Sequence 1, Appli
12	43	43.4	265	4	US-03-270-767-47089 Sequence 1, Appli
13	43	43.4	311	4	US-03-270-767-48661 Sequence 1, Appli
14	42	42.4	187	4	US-03-248-796A-20325 Sequence 1, Appli
15	42	42.4	358	4	US-03-540-236-3758 Sequence 1, Appli
16	42	42.4	1190	4	US-03-252-991A-21474 Sequence 1, Appli
17	41	41.4	120	4	US-03-252-991A-26719 Sequence 1, Appli
18	41	41.4	155	4	US-03-248-796A-14464 Sequence 1, Appli
19	41	41.4	166	4	US-03-134-000C-4868 Sequence 1, Appli
20	41	41.4	326	3	US-03-089-000C-37A-11 Sequence 1, Appli
21	41	41.4	326	6	5395759-2 Sequence 1, Appli
22	41	41.4	365	4	US-03-248-796A-18622 Sequence 1, Appli
23	41	41.4	817	4	US-03-248-796A-17089 Sequence 1, Appli
24	41	41.4	1455	3	US-03-840-062-5 Sequence 1, Appli
25	41	41.4	1464	2	US-03-231-193A-11 Sequence 1, Appli
26	41	41.4	1464	3	US-03-486-273A-11 Sequence 1, Appli
27	41	41.4	1464	3	US-03-940-086A-11 Sequence 1, Appli

101 38 38.4 535 3 US-03-286-870A-6 Sequence 6, Appli  
 102 38 38.4 543 2 US-03-922-170B-10 Sequence 10, Appli  
 103 38 38.4 543 3 US-03-071-739B-2 Sequence 2, Appli  
 104 38 38.4 543 3 US-03-181-336-13 Sequence 13, Appli  
 105 38 38.4 543 3 US-03-260-038B-2 Sequence 2, Appli  
 106 38 38.4 543 4 US-03-635-922-2 Sequence 2, Appli  
 107 38 38.4 543 4 US-03-487-716A-2 Sequence 2, Appli  
 108 38 38.4 543 4 US-03-322-977-2 Sequence 2, Appli  
 109 38 38.4 543 4 US-03-186-200-1 Sequence 1, Appli  
 110 38 38.4 543 4 US-03-435-739-10 Sequence 10, Appli  
 111 38 38.4 543 4 US-03-930-218-3 Sequence 3, Appli  
 112 38 38.4 543 4 US-03-704-772A-2 Sequence 2, Appli  
 113 38 38.4 543 4 US-03-988-113-10 Sequence 10, Appli  
 114 38 38.4 545 4 US-03-893-4 0-18 Sequence 18, Appli  
 115 38 38.4 545 4 US-03-328-352-920 Sequence 4920, Appli  
 116 38 38.4 547 2 US-03-642-684-2 Sequence 2, Appli  
 117 38 38.4 547 3 US-03-157-397-2 Sequence 1, Appli  
 118 38 38.4 547 4 US-03-512-021-2 Sequence 2, Appli  
 119 38 38.4 547 4 US-03-512-021-2 Sequence 10, Appli  
 120 38 38.4 548 3 US-03-157-397-4 Sequence 18, Appli  
 121 38 38.4 548 4 US-03-601-777-2 Sequence 2, Appli  
 122 38 38.4 548 4 US-03-512-021-4 Sequence 2, Appli  
 123 38 38.4 549 2 US-03-642-684-4 Sequence 4, Appli  
 124 38 38.4 549 4 US-03-435-739-14 Sequence 4, Appli  
 125 38 38.4 549 4 US-03-988-113-14 Sequence 14, Appli  
 126 38 38.4 561 4 US-03-071-035-468 Sequence 466, App  
 127 38 38.4 564 3 US-03-286-870A-4 Sequence 468, App  
 128 38 38.4 565 4 US-03-248-796A-14308 Sequence 4, Appli  
 129 38 38.4 567 4 US-03-09-710-279-322 Sequence 3022, Ap  
 130 38 38.4 571 4 US-03-286-870A-8 Sequence 8, Appli  
 131 38 38.4 575 3 US-03-134-001C-3681 Sequence 3681, AP  
 132 38 38.4 576 3 US-03-248-796A-15566 Sequence 15566, A  
 133 38 38.4 594 4 US-03-570-856B-31 Sequence 31, Appli  
 134 38 38.4 602 4 US-03-09-248-796A-14503 Sequence 14503, A  
 135 38 38.4 617 4 US-03-071-035-458 Sequence 458, App  
 136 38 38.4 624 4 US-03-09-071-035-462 Sequence 462, App  
 137 38 38.4 634 4 US-03-134-001C-6612 Sequence 6612, AP  
 139 38 38.4 646 2 US-03-822-445-2 Sequence 2, Appli  
 140 38 38.4 656 3 US-03-396-540-1 Sequence 2, Appli  
 141 38 38.4 666 3 US-03-206-936-1 Sequence 30, Appli  
 142 37.5 37.9 262 3 US-03-08-961-083-30 Sequence 30, Appli  
 143 37.5 37.9 262 4 US-03-536-784-30 Sequence 4, Appli  
 144 37.5 37.9 262 4 US-03-599-632-4 Sequence 448, App  
 145 37.5 37.9 262 4 US-03-198-452A-448 Sequence 4528, AP  
 146 37.5 37.9 262 4 US-03-09-543-681A-4528 Sequence 21, Appli  
 147 37.5 37.9 263 3 US-03-091-725-21 Sequence 22, Appli  
 148 37.5 37.9 263 4 US-03-691-270A-22 Sequence 38359, A  
 149 37.5 37.9 279 4 US-03-270-767-38329 Sequence 53546, A  
 150 37.5 37.9 279 4 US-03-270-767-38346 Sequence 53546, A

## ALIGNMENTS

COUNTRY: USA  
 ZIP: 02142  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/197,970B  
 FILING DATE: 23-Nov-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/018,228  
 FILING DATE: 24-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Levine, Leslie M.  
 REGISTRATION NUMBER: 35,245  
 REFERENCE/DOCKET NUMBER: A010 PCT CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 679-2810  
 TELEFAX: (617) 679-2838  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 334 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-197-970B-7

Query Match: 100.0%; Score: 99; DB: 4; Length: 334;  
 Best Local Similarity: 100.0%; Pred. No.: 5; 8e-08;  
 Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 SSDGLANNNNTQQLPHEH 18  
 DB 264 SSDGLANNNNTQQLPHEH 281

RESULT 2  
 US-08-287-001A-2  
 ; Sequence 2, Application US/08287001A  
 ; GENERAL INFORMATION:  
 ; Patent No. 5622861  
 ; APPLICANT: KAPLAN, GERRARDO  
 ; APPLICANT: FRINSTONE, STEPHEN M.  
 ; TITLE OF INVENTION: HEPATITIS A VIRUS RECEPTOR AND METHODS  
 ; TITLE OF INVENTION: OF USE  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
 ; STREET: Suite 1200, The Candler Bldg, 127 Peachtree  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30303

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/287,001A  
 FILING DATE:  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Spratt, Gwendolyn D.  
 REGISTRATION NUMBER: 36,016  
 REFERENCE/DOCKET NUMBER: 1414-621  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404/688-9880  
 TELEFAX: 404/688-9880

RESULT<sup>1</sup>  
 US-09-197-970B-7  
 ; Sequence 7, Application US/09197970B  
 ; Patent No. 666485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michele Sanicola-Nadel  
 ; Joseph V. Bonventre  
 ; Catherine A. Hession  
 ; Takaharu Ichimura  
 ; Henry Wei  
 ; Richard L. Cate  
 ; TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Biogen, Inc.  
 ; STREET: 14 Cambridge Center  
 ; CITY: Cambridge  
 ; STATE: MA

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-287-001A-2

Query Match 84.8%; Score 84; DB 1; Length 451;  
 Best Local Similarity 88.9%; Pred. No. 2e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSDGIVNNNNTQLFLEHS 18  
 Db 344 SSDGIVNNNNTQLFLEHS 361

RESULT 3

PCT-US95-09941-2

Sequence 2, Application PC/TUS9509941

GENERAL INFORMATION:

APPLICANT: HEPATITIS A VIRUS RECEPTOR AND METHODS

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDIE &amp; ROSENBERG, P.C.

STREET: Suite 1200, The Candler Bldg, 127 Peachtree

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09941

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/287,001

FILING DATE: 5 AUG 1994

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414.621

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404/688-0770

TELEFAX: 404/688-9880

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 84.8%; Score 84; DB 1; Length 451;  
 Best Local Similarity 88.9%; Pred. No. 2e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 344 SSDGIVNNNNTQLFLEHS 361

## GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 1017196.132

CURRENT APPLICATION NUMBER: US/09/248,76A

CURRENT FILING DATE: 1995-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15079

LENGTH: 570

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-15079

Query Match 52.5%; Score 52; DB 4; Length 570;  
 Best Local Similarity 57.1%; Pred. No. 3.2.;  
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 SDGLMNNNNTQLF 15  
 Db 2 NDGIMNNNDLFL 15

RESULT 5

US-09-991-258-13

Sequence 13, Application US/09991258

PATENT NO. 6783939

GENERAL INFORMATION:

APPLICANT: Olmsted, Robert

APPLICANT: Keith, Paula

APPLICANT: Dryga, Sergey

APPLICANT: Caley, Ian

APPLICANT: Maughan, Maureen

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

APPLICANT: Johnston, Robert

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Ronald

Query Match 48.5%; Score 48; DB 4; Length 981;  
 Best Local Similarity 50.0%; Pred. No. 26;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSDGIVNNNNTQLFLEHS 16  
 Db 489 SLDHLWNQQMFWIQ 504

RESULT 4  
 US-09-248-796A-15079  
 Sequence 1079, Application US/09248796A  
 Patent No. 6747137

; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
 ; IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 43  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/1185, 670  
 ; FILING DATE: 21-JAN-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 986, 931  
 ; FILING DATE: 08-DEC-1992  
 ; APPLICATION NUMBER: 808, 122  
 ; FILING DATE: 16-DEC-1991  
 ; APPLICATION NUMBER: 440, 625  
 ; FILING DATE: 22-NOV-1989  
 ; APPLICATION NUMBER: 315, 015  
 ; FILING DATE: 23-FEB-1989  
 ; SEQ ID NO:13: LENGTH: 114  
 ; 5514582-13

Query Match Best Local Similarity 45.5%; Score 45; DB 6; Length 114;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SDGLWNNNQTO 12  
 Db 97 SDGLWNDNFCCQ 107

RESULT 7

5514582-14

; Patent No. 5514582

; PRIORITY:

; CARON, DANIEL J.; LASKY, LAURENCE A.

; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID

; IMMUNOGLOBULINS

; NUMBER OF SEQUENCES: 43

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/1185, 670

; FILING DATE: 21-JAN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 986, 931

; FILING DATE: 08-DEC-1992

; APPLICATION NUMBER: 808, 122

; FILING DATE: 16-DEC-1991

; APPLICATION NUMBER: 440, 625

; FILING DATE: 22-NOV-1989

; APPLICATION NUMBER: 315, 015

; FILING DATE: 23-FEB-1989

; SEQ ID NO:14: LENGTH: 114

; 5514582-14

RESULT 8

US-08-026-138B-1

; Sequence 1, Application US/08026138B

; Patent No. 5502166

; GENERAL INFORMATION:

; APPLICANT: Mishina, Masayoshi

; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538, 092

; PRIOR APPLICATION NUMBER: 60/127, 352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178, 965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqFormatter Version 0.9

; SEQ ID NO: 967

; LENGTH: 590

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

COUNTRY: JAPAN  
 ZIP: 951  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS v.5  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/026, 138B  
 FILING DATE: 26-FEB-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 39563/1992  
 FILING DATE: 26-FEB-1992  
 APPLICATION NUMBER: JP 17315/1992  
 FILING DATE: 30-JUN-1992  
 APPLICATION NUMBER: JP 215017/1992  
 FILING DATE: 12-AUG-1992  
 APPLICATION NUMBER: JP 303878/1992  
 FILING DATE: 13-NOV-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamburg, C.Bruce  
 REGISTRATION NUMBER: 22, 389  
 REFERENCE/DOCKET NUMBER: P-4551  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 956-2340  
 FAX: (212) 953-7733  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 STRANDBEDNESS: single strand  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: mouse  
 TISSUE TYPE: cerebellum  
 PUBLICATION INFORMATION:  
 AUTHORS: Masayoshi MISHINA  
 TITLE: NOVEL PROTEINS AND GENES CODING THE SAME  
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464

US-08-026-138B-1

Query Match

Best Local Similarity

45.5%; Score

45; DB 6;

Length 114;

Matches

8; Conservative

1; Mismatches

2; Indels

0; Gaps

0;

Db

1174 NEDGLPNNDQYKLYAH

1190

US-09-538-092-967

Query Match

Best Local Similarity

45.5%; Score

45; DB 1;

Length 1464;

Matches

8; Conservative

5; Mismatches

4; Indels

0; Gaps

0;

Db

1174 NEDGLPNNDQYKLYAH

1190

RESULT 9

US-09-538-092-967

; Sequence 967, Application US/9538092

; Patent No. 675314

; GENERAL INFORMATION:

; APPLICANT: Giot, Loic

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538, 092

; PRIOR APPLICATION NUMBER: 60/127, 352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178, 965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqFormatter Version 0.9

; SEQ ID NO: 967

; LENGTH: 590

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P20309
US-09-538-092-967

Query Match    44.4%; Score 44; DB 4; Length 590;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy      1 SDSGIWNNNOTQOLFLEHS 18
Db      332 SSSLSWNNDAAASLENS 349

RESULT 10
US-09-248-796A-22793
; Sequence 22793, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ_ID NO 22793
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22793

Query Match    43.4%; Score 43; DB 4; Length 62;
Best Local Similarity 47.1%; Pred. No. 7.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      2 SDGILWNNNQTOQOLFLEHS 18
Db      25 SDSIQLQPTVNLVLPYQHS 41

RESULT 11
US-09-270-767-49147
; Sequence 49147, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ_ID NO 48661
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-48661

Query Match    43.4%; Score 43; DB 4; Length 311;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy      5 LWNNN--QTOQOLFLEHS 18
Db      141 LWNNNYQKTRLFRKNS 156

RESULT 14
US-09-248-796A-20325
; Sequence 20325, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ_ID NO 20325
; LENGTH: 187

RESULT 12

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; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20325
Query Match 42.4%; Score 42; DB 4; Length 187;
Best Local Similarity 60.0%; Pred. No. 36; Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 SDGLWNNNQTLFL 15
Db 9 SSLGLWNKHAKLFL 23

RESULT 15
US-09-540-236-3758
Sequence 3758, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Keith Wainstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26719
; LENGTH: 120
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3758

Query Match 42.4%; Score 42; DB 4; Length 358;
Best Local Similarity 63.6%; Pred. No. 75; Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 GLWNNNQTLF 14
Db 80 GLWNNDEQECAF 90

RESULT 16
US-09-232-991A-21474
Sequence 21474, Application US/09232991A
; Patent No. 65195
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21474
; LENGTH: 1190
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-232-991A-21474

RESULT 17
US-09-248-796A-26719
Query Match 42.4%; Score 42; DB 4; Length 1190;
Best Local Similarity 50.0%; Pred. No. 2.9e+02; Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 SDGLWNNNQTL 13
Db 346 TDGLWNNDSAV 357

RESULT 17
US-09-248-796A-26719

RESULT 18
US-09-248-796A-14464
Sequence 14464, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14464
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14464

Query Match 41.4%; Score 41; DB 4; Length 155;
Best Local Similarity 46.7%; Pred. No. 42; Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 3 DGLWNNNQTLFLH 17
Db 29 DKVWKVNTQVOEN 43

RESULT 19
US-09-134-000C-4868
Sequence 4868, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032196-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-15

```

NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 4868  
 LENGTH: 166  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-4868

Query Match 41.4%; Score 41; DB 4; Length 166;  
 Best Local Similarity 53.8%; Pred. No. 46;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SDGLMNNNQTLF 14  
 Db 86 SDRTWNNYTBIF 98

RESULT 20

US-08-397A-11  
 Sequence 11, Application US/08089397A  
 Patent No. 6086880  
 GENERAL INFORMATION:

APPLICANT: FABBARA, MARTA I.J.  
 APPLICANT: FRENCHICK, PATRICK J.  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: LAZ, MOHAMMAD K.

APPLICANT: GILCHRIST, JAMES E.  
 APPLICANT: REDMOND, MARK J.  
 TITLE OF INVENTION: ROTAVIRUS VACCINES

NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 2000 Pennsylvania Avenue, NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1888

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/089, 397A  
 FILING DATE: 07-JUL-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: ADLER, REID G.  
 REGISTRATION NUMBER: 30, 988  
 REFERENCE/DOCKET NUMBER: 29311-20003.03  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 87-1500  
 TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 326 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-089-397A-11

Query Match 41.4%; Score 41; DB 3; Length 326;  
 Best Local Similarity 57.1%; Pred. No. 98;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDGLMNNNQTLF 15  
 Db 94 SDDEWENTISQFL 107

Patent No. 5395759  
 APPLICANT: HOLMES, TAN H.; DYALL-SMITH, MICHAEL L.  
 TITLE OF INVENTION: DNA SEQUENCES AND AMINO ACID SEQUENCE  
 ENCODING THE HUMAN ROTAVIRUS MAJOR OUTER CAPSID GLYCOPROTEIN  
 NUMBER OF SEQUENCES: 14  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/474, 642  
 FILING DATE: 29-APR-1985  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 834, 704  
 FILING DATE: 04-FEB-1987  
 SEQ ID NO: 2:  
 LENGTH: 326  
 5395759-2

Query Match 41.4%; Score 41; DB 6; Length 326;  
 Best Local Similarity 57.1%; Pred. No. 98;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDGLMNNNQTLF 15  
 Db 94 SDDEWENTISQFL 107

RESULT 22

US-09-248-796A-18622  
 Sequence 18622, Application US/09248796A  
 Patent No. 6747137  
 GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196-132  
 CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096, 409

NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 18622

LENGTH: 365

TYPE: PRT  
 ORGANISM: Candida albicans

US-09-248-796A-18622

Query Match 41.4%; Score 41; DB 4; Length 365;  
 Best Local Similarity 53.8%; Pred. No. 1.1e-02;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 GLWNNTATDFNIE 291  
 Db 279 GLWNNTATDFNIE 291

RESULT 23

US-09-248-796A-17089  
 Sequence 17089, Application US/09248796A  
 Patent No. 6747137  
 GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196-132  
 CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR FILING DATE: 1998-08-13  
 NUMBER OF SEQ ID NOS: 28208

RESULT 21  
 5395759-2

TYPE: PRT  
 ORGANISM: Candida albicans  
 US-09-248-796A-17089

Query Match 41.4%; Score 41; DB 4; Length 817;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSDGIWNNNOTQLF 14  
 Db 327 SIDKUWNDNPVYIF 340

RESULT 24  
 US-08-840-062-5  
 Sequence 5, Application US/08840062  
 Patent No. 6117977  
 GENERAL INFORMATION:  
 APPLICANT: WU, KAI  
 TITLE OF INVENTION: TYPE C LECTINS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 APPLICATION NUMBER: US/08/840,062

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/840,062

FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Ginger R.  
 REGISTRATION NUMBER: 33,055  
 REFERENCE/DOCKET NUMBER: P1019R1

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-3216  
 TELEFAX: 415/932-9881  
 TELEX: 910371-7168

INFORMATION FOR SEQ ID NO: 5:  
 LENGTH: 1455 amino acids  
 SEQUENCE CHARACTERISTICS:  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

US-08-840-062-5

Query Match 41.4%; Score 41; DB 3; Length 1455;  
 Best Local Similarity 87.5%; Pred. No. 5.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 1 SSDGIWNN 8  
 Db 1335 SSSGIWNN 1342

RESULT 25  
 US-08-231-193A-11  
 Sequence 11, Application US/08231193A  
 Patent No. 5849805  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92101-2926

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,273A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435

---

NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,273A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/231,193  
 FILING DATE: 20-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REFERENCE/DOCKET NUMBER: 33,779  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 TYPE: amino acid  
 US-08-436-273A-11

RESULT 27  
 US-08-940-085A-11  
 Sequence 11, Application US/08940086A  
 Patent No. 6111091  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Liu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller, Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,332B  
 FILING DATE: 10-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YABLONSKY, MICHAEL D.  
 REGISTRATION NUMBER: 40,407  
 REFERENCE/DOCKET NUMBER: T1210Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4678  
 TELEFAX: 732-594-4720  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-436-332B-10

RESULT 28  
 US-08-436-332B-10  
 Sequence 10, Application US/08436332B  
 Patent No. 6130058  
 GENERAL INFORMATION:  
 APPLICANT: LE BOURDELLES, BEATRICE  
 APPLICANT: MEERS, BEATRICE  
 APPLICANT: WHITING, PAUL JOHN  
 TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING NMDA RECEPTORS, AND NOVEL CLONED NMDA RECEPTOR SUBUNIT SEQUENCES  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.  
 STREET: 126 EAST LINCOLN AVE., - P.O. BOX 2000  
 CITY: Rahway  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07065  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,332B  
 FILING DATE: 10-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YABLONSKY, MICHAEL D.  
 REGISTRATION NUMBER: 40,407  
 REFERENCE/DOCKET NUMBER: T1210Y  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-4678  
 TELEFAX: 732-594-4720  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-436-332B-10

RESULT 29  
 US-08-940-035A-11  
 Sequence 11, Application US/08940035A  
 Patent No. 631661  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.

CURRENT APPLICATION DATA:  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/940,035A  
 FILING DATE: 29-SEPT-97  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/231,193  
 FILING DATE: 20-APR-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/052,449  
 FILING DATE: 20-APR-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0962

INFORMATION FOR SEQ ID NO: 11:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

RESULT 30  
 US-08-935-105A-11  
 Query Match Score 41; DB 3; Length 1464;  
 Sequence 11, Application US/09648797  
 Best Local Similarity 41.4%; Pred. No. 5,3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY : :|||:||:||:||:  
 Db 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 31  
 US-09-643-797-11  
 Query Match Score 41; DB 3; Length 1464;  
 Sequence 11, Application US/09648797  
 Best Local Similarity 41.2%; Pred. No. 5,3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY : :|||:||:||:||:  
 Db 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 32  
 US-09-643-797-11  
 Query Match Score 41; DB 3; Length 1464;  
 Sequence 11, Application US/09648797  
 Best Local Similarity 41.2%; Pred. No. 5,3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY : :|||:||:||:||:  
 Db 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 33  
 US-08-935-105A-11  
 Sequence 11, Application US/08935105A  
 PATENT NO. 6376660

GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Lu, Chin-Chun  
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Heller Ehman White & McAuliffe  
 STREET: 4250 Executive Square, 7th Floor  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/648,797  
 FILING DATE: 28-APR-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/940,086A  
 FILING DATE: 29-SEPT-97  
 APPLICATION NUMBER: US/08/231,193  
 FILING DATE: 20-APR-1994

APPLICATION NUMBER: US/08/052,449  
 FILING DATE: 20-APR-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 24735-9383C  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 450-8400  
 TELEFAX: (619) 450-8499  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Query Match 41.4%; Score 41; DB 4; Length 1464;  
 Best Local Similarity 41.2%; Pred. No. 5.3e+02;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQQLFLEH 17  
 DB 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 32

US-08-217-704C-2  
 ; Sequence 2, Application US/08217704C  
 ; Patent No. 6489124  
 GENERAL INFORMATION:  
 APPLICANT: Foldes, Robert  
 Fantaske, Robert  
 Adams, Sally-Lynn  
 Kamboj, Rajender  
 TITLE OF INVENTION: MODULATORY PROTEINS OF HUMAN CNS  
 RECEPIORS  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street  
 CITY: Washington, D.C., N.W.  
 COUNTRY: USA  
 ZIP: 20007-5109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/386,123  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/987,953  
 FILING DATE: 11-DEC-94  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 16777/259/ALB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1464 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 US-08-217-704C-2

RESULT 33  
 US-09-386-123-11  
 ; Sequence 11, Application US/09386123  
 ; Patent No. 6521413  
 GENERAL INFORMATION:  
 APPLICANT: Daggett, Lorrie P.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Liaw, Chen W.  
 APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION:

SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Einman White &amp; McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/386,123

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,449

FILING DATE: 20-APR-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383F

TELECOMMUNICATION INFORMATION:

TELEPHONE: 858-450-8403

TELEFAX: 858-587-5360

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1464 amino acids

TOPOLGY: linear

MOLECULE TYPE: protein

US-09-386-123-11

RESULT 34  
 US-09-187-049-8  
 ; Sequence 8, Application US/09187049  
 ; Patent No. 631766  
 GENERAL INFORMATION:  
 APPLICANT: Lampka, Gayle K.

TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME

TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-217-704C-2

Query Match 41.4%; Score 41; DB 4; Length 1464;

Best Local Similarity 41.2%; Pred. No. 5.3e+02;

Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQQLFLEH 17

DB 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 34

US-09-187-049-8

; Sequence 8, Application US/09187049

; Patent No. 631766

GENERAL INFORMATION:

APPLICANT: Lampka, Gayle K.

TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME

TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-217-704C-2

Query Match 41.4%; Score 41; DB 4; Length 1464;

Best Local Similarity 41.2%; Pred. No. 5.3e+02;

Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQQLFLEH 17

DB 1174 NEEGLSNNDQYKLYSKH 1190

RESULT 34

US-09-187-049-8

; Sequence 8, Application US/09187049

; Patent No. 631766

GENERAL INFORMATION:

APPLICANT: Lampka, Gayle K.

TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME

TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-217-704C-2

Query Match 41.4%; Score 41; DB 4; Length 1464;

Best Local Similarity 41.2%; Pred. No. 5.3e+02;

Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQQLFLEH 17

DB 1174 NEEGLSNNDQYKLYSKH 1190

ADDRESSEE: BRINKS HOFER GILSON & LIONE  
 STREET: P.O. Box 10395  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60610

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/187,049  
 FILING DATE: 2000-03-24  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/695,177  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Martin, Alice O.  
 REGISTRATION NUMBER: 35,601  
 REFERENCE/DOCKET NUMBER: 7814/16  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312 321-4200  
 TELEFAX: 312 321-4299  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 124 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: MPP B subunit from rat  
 US-09-187,049-8

RESULT 35  
 Query Match 40.4%; Score 40; DB 3; Length 124;  
 Best Local Similarity 41.7%; Pred. No. 48; Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;  
 Qy 4 GLW-----NNNQTLFLEH 17  
 Db 20 GLWIDAGSRYENENKGNTAHFLEH 43

RESULT 36  
 Query Match 40.4%; Score 40; DB 3; Length 124;  
 Best Local Similarity 41.7%; Pred. No. 48; Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;  
 Qy 4 GLW-----NNNQTLFLEH 17  
 Db 82 GLWIDAGSRYENENKGNTAHFLEH 105

RESULT 37  
 US-09-248-796A-16186  
 Sequence 16186, Application US/09248796A  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 FILE REFERENCE: 107196.132  
 CURRENT APPLICATION NUMBER: US/09/248,796A  
 CURRENT FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409  
 PRIOR FILING DATE: 1998-08-13  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 16186  
 LENGTH: 186  
 TYPE: PRT  
 ORGANISM: Candida albicans  
 US-09-248-796A-16186

RESULT 38  
 US-08-807-263-4  
 Sequence 4, Application US/08007263C  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Mortensen, Uffe  
 APPLICANT: Olesen, Kjeld  
 APPLICANT: Steinicke, Henning  
 APPLICANT: Sorensen, Steen B.  
 APPLICANT: Breedam, Klaus  
 TITLE OF INVENTION: MODIFIED CARBOXYPEPTIDASE

Query Match 40.4%; Score 40; DB 4; Length 126;  
 Best Local Similarity 43.8%; Pred. No. 48; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Qy 3 DGLWMNNQTLFLEHS 18  
 Db 95 DGVVYTNTGDOFVEHS 110

RESULT 36

FILE REFERENCE: 8648.71us01-no4  
; CURRENT APPLICATION NUMBER: US/08/807,263C  
; CURRENT FILING DATE: 1997-02-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 4  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: *Saccharomyces cerevisiae*  
; US-08-807-263-4

Query Match 40.4%; Score 40; DB 2; Length 421;  
; Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
; Qy 6 WNNNOTQFLEH 16  
; Db 84 WNSNATWIEFD 94

RESULT 39  
US-09-375-140-10  
; Sequence 10, Application US/09375140  
; PatenT No. 6489540  
; GENERAL INFORMATION:  
; APPLICANT: Kavanagh, T.  
; TITLE OF INVENTION: A NOVEL PLASTID-TARGETING NUCLEAR ACID SEQUENCE, A STIMULUS-RESPONSIVE TITLE OF INVENTION: PROMOTER AND USES THEREOF  
; FILE REFERENCE: 9341-017  
; CURRENT APPLICATION NUMBER: US/09/375,140  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 10  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: *Arabidopsis thaliana*  
; US-09-375-140-10

Query Match 40.4%; Score 40; DB 4; length 463;  
; Best Local Similarity 42.9%; Pred. No. 2.1e+02;  
; Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DGLMANNNOTQFLEH 16  
; Db 242 DGTMNSEYGFEME 255

RESULT 40  
US-08-895-521-1  
; Sequence 1, Application US/08895521  
; PatenT No. 5869311  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: MITOCHONDRIAL PROCESSING PEPTIDASE  
; TITLE OF INVENTION: SUBUNIT  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/895,521  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0343 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-655-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 amino acids  
; STRANDEDNESS: single  
; IMMEDIATE SOURCE:  
; LIBRARY: BRAIN014  
; CLONE: 1533490  
; US-08-895-521-1

Query Match 40.4%; Score 40; DB 2; Length 489;  
; Best Local Similarity 41.7%; Pred. No. 2.2e+02;  
; Matches 10; Conservative 0; Mismatches 4; Indels 10; Gaps 1;  
; Qy 4 GLW-----NNNOTQFLEH 17  
; Db 82 GLWIDAGSRVENEKONGTARHFLEH 105

Search completed: December 30, 2004, 16:14:38  
Job time : 40 secs

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Run on:	December 30, 2004, 16:03:35 ; Search time 190 Seconds	Search time 190 Seconds
<b>OM protein - protein search, using sw model</b>		
Title:	US-10-718-321-1	32
Perfect score:	99	49
Sequence:	1 SSDGLWNNNQTLFLEHS 18	48.5
Scoring table:	BLOSUM62	33
Gapop 10.0 , Gapext 0.5	48	
Searched:	1825181 seqs, 575374646 residues	48
Total number of hits satisfying chosen parameters:	1825181	48
Minimum DB seq length: 0	48	
Maximum DB seq length: 200000000	48	
Post-processing: Minimum Match 0%	48	
listing first 150 summaries	48	
Database :		48
1: UniProt_02:*	48	
2: uniprot_sprot:*	48	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	48	
<b>SUMMARIES</b>		
Result No.	Score	Query Match length DB ID Description
1	99	100.0 359 2 043656 homo sapien
2	99	100.0 364 2 096d42 homo sapien
3	99	100.0 364 2 CAG33395 homo sapien
4	84	84.8 451 2 095144 cercopithecus aethiops
5	84	84.8 460 2 018984 cercopithecus aethiops
6	84	84.8 469 2 QTJ748 cercopithecus aethiops
7	84	84.8 473 2 QTJJ47 cercopithecus aethiops
8	84	84.8 474 2 046597 cercopithecus aethiops
9	84	84.8 478 2 046598 cercopithecus aethiops
10	51	51.5 392 1 CEMA_NEPOL nephrosemili
11	49	49.5 267 2 QBZS98 anabena sp
12	49	49.5 278 1 CEMA_GUTH guillardia
13	49	49.5 338 2 P73105 synchocystis
14	48	48.5 129 2 Q8BRW1 obstrum
15	48	48.5 416 1 HAPC_PIG mus musculus
16	48	48.5 558 2 036293 sus scrofa
17	48	48.5 558 2 036294 venezuelan
18	48	48.5 559 2 036297 venezuelan
19	48	48.5 559 2 036298 venezuelan
20	48	48.5 559 2 036308 venezuelan
21	48	48.5 559 2 036309 venezuelan
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23	48	48.5 559 2 Q9WCFF9 venezuelan
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25	48	48.5 559 2 Q98755 venezuelan
26	48	48.5 559 2 Q8V5J7 venezuelan
27	48	48.5 559 2 Q8V5J8 venezuelan
28	48	48.5 1254 1 POLS_BEVVB venezuelan
29	48	48.5 1254 1 POLS_BEVVE venezuelan
30	48	48.5 1254 1 POLS_BEVVT venezuelan
31	48	48.5 1254 2 Q77VY8 venezuelan

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GenCore version 5.1.6

09YKCA4 venezuelan  
Aadi4551 venezuelan  
P36329 venezuelan  
P36332 venezuelan  
036287 venezuelan  
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09wcr1 venezuelan  
06cb54 yarrowia li  
09wc27 venezuelan  
098773 venezuelan  
098775 venezuelan  
09YKCS5 venezuelan  
09YKCF7 venezuelan  
07YD94 echinops te  
093289 echinops te  
075021 human immun  
075022 human immun  
09wn97 streptomyce  
P08290 rattus norvegicus  
094au9 solanum tuberosum  
08159 oryza sativa  
09c55 arabidopsis  
09hms homosapiens  
09xcl8 bacteroides  
098k4 pseudomonas  
06fhl3 candida glabrata  
1NME1\_MOUSE

Q94au9 solanum tuberosum  
08159 oryza sativa  
09c55 arabidopsis  
09hms homosapiens  
09xcl8 pseudomonas  
06fhl3 candida glabrata  
P36336 mus musculus  
Q00599 rattus norvegicus  
008948 rattus norvegicus  
Baa01069 mus musculus  
Q9m89 rhizobium m  
Q9ek18 ovis aries  
Q75012 human immunogen  
Q75014 human immunoglobulin  
Q75015 human immunoglobulin  
Q9muu7 mesostigma  
Q81615 meriones unguiculatus  
Q72n84 leptospira  
Q8ffcc3 leptospira  
Aa871503 leptospiral  
Q79q4 banditatus  
Q6j3z8 bartonella  
Q6164 bartonella  
Q827j3 enterococcus  
Q8w108 psilotum nudum  
Q72vfl1 desulfobacter  
Aa894396 desulfobacter  
Q6ccv9 yarrowia li  
Q7371 ashbya gossypii  
Aa852706 ashbya go  
Q7rxnb neurospora  
Q96r699 homo sapiens  
Q61994 homo sapiens  
Baa19019 homo sapiens  
ACM3\_MOUSE  
P08483 rattus norvegicus

105	44	44.4	589	2	BAC39088	Bac3-8088 mus muscu	DR GO; GO:0004872; F-receptor activity; IEA.
106	44	44.4	590	1	ACM3_BOVIN	P41984 bov taurus	DR InterPro; IPR003399; IG.
107	44	44.4	590	1	ACM3_GORGO	Q9na33 gorilla gor	DR InterPro; IPR007110; IG-like.
108	44	44.4	590	1	ACM3_HUMAN	P20309 homo sapien	DR InterPro; IPR003066; IG_MHC.
109	44	44.4	590	1	ACM3_PANTR	Q9n2a4 pan troglod	DR Pfam; PF0047; Ig; 1.
110	44	44.4	590	1	AQM3_PIG	P11483 sus scrofa	DR SMART; SM00419; Ig; 1.
111	44	44.4	590	1	ACM3_PONY	Q9n2a2 pongo pygma	DR PROSITE; PS00835; IG_LIKE; 1.
112	44	44.4	639	1	ACM3_CHICK	P49578 gallus galli	DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
113	44	44.4	664	2	O9AQE5	P0861w2 dictyostelia	KW Receptor.
114	44	44.4	681	2	O7AAPO	Q9sges5 bacillus sp	DR SEQUENCE 359 AA; 38704 MW; C207FHC562DC62CA CRC64;
115	44	44.4	964	2	O47170	Q47170 escherichia	DR 086728 streptomyce
116	44	44.4	973	2	O87278	Q7bsv0 shigella fl	DR Best local similarity 100.0%; Pred. No. 3.1e-0%; Mismatches 0; Indels 0; Gaps 0;
117	44	44.4	1028	2	O7BZV0	Q8sg39 shigella fl	DR Matches 18; Conservativity 100.0%; Pred. No. 3.1e-0%; Mismatches 0; Indels 0; Gaps 0;
118	44	44.4	1028	2	O83Q39	P08664 escherichia	DR 086728 shigella fl
119	44	44.4	1030	1	BGA2_ECOLI	P08664 escherichia	DR 086728 shigella fl
120	44	44.4	1030	2	O6BF50	Q6bf50 escherichia	DR 086728 shigella fl
121	44	44.4	1042	2	O7AAPO	Q7aaeo escherichia	DR 086728 shigella fl
122	44	44.4	1042	2	O8XAM9	Q8xam9 escherichia	DR 086728 shigella fl
123	44	44.4	1084	2	O9PR18	Q9pr18 ureaplasma	DR 086728 shigella fl
124	44	44.4	1084	2	O8FDFO	Q8fdfo escherichia	DR 086728 shigella fl
125	44	44.4	1138	2	O81KV6	Q8a3n1 bacteroides	DR 086728 shigella fl
126	44	44.4	1138	2	O7DQZ9	Q9q760 human immun	DR 086728 shigella fl
127	43	43.4	115	2	O9Q760	Q8hd87 carteria ob	DR 086728 shigella fl
128	43	43.4	118	2	O8HBD7	Q70629 human immun	DR 086728 shigella fl
129	43	43.4	171	2	O7DQZ9	Cad87143 human imm	DR 086728 shigella fl
130	43	43.4	171	2	O4D87143	Q9g946 babicilamys	DR 086728 shigella fl
131	43	43.4	227	2	O9GH46	P74730 synechocyst	DR 086728 shigella fl
132	43	43.4	254	2	O74730	Q57488 rotavirus a	DR 086728 shigella fl
133	43	43.4	325	2	O9TQ99	Q9g999 shinisurus	DR 086728 shigella fl
134	43	43.4	345	2	O9TQ99	Q7xc88 oryza sativ	DR 086728 shigella fl
135	43	43.4	422	2	O7XPC8	Q76199 chlamydom	DR 086728 shigella fl
136	43	43.4	454	2	O8HDB6	Q8ihab pseudocarote	DR 086728 shigella fl
137	43	43.4	464	2	O8HDB9	Q8hd99 carteria ra	DR 086728 shigella fl
138	43	43.4	464	2	O8HDD1	Q8hd11 chlamydomon	DR 086728 shigella fl
139	43	43.4	464	2	O8HDD2	Q8hd22 chlamydomon	DR 086728 shigella fl
140	43	43.4	464	2	O8HDD6	Q8hd6 pediasrium	DR 086728 shigella fl
141	43	43.4	464	2	O8HDD6	Bac87678 chlamyd	DR 086728 shigella fl
142	43	43.4	464	2	O8HDD7	Q9upj0 hydra atten	DR 086728 shigella fl
143	43	43.4	484	2	O9U9P0	Q8luq6 vitreochlam	DR 086728 shigella fl
144	43	43.4	498	2	O8LUQ6	Q8mb7 vitreochlam	DR 086728 shigella fl
145	43	43.4	498	2	O8MBP7	Q9gh48 tetrabenea	DR 086728 shigella fl
146	43	43.4	498	2	O9GH48	Q7sy19 brachydanio	DR 086728 shigella fl
147	43	43.4	516	2	O7SY19	Q7pym5 opophelus g	DR 086728 shigella fl
148	43	43.4	516	2	O7PYM5	Q6pdm4 Q6pm4	DR 086728 shigella fl
149	43	43.4	579	2	OAH58624	Aah58624 mus muscu	DR 086728 shigella fl
<b>ALIGNMENTS</b>							
<b>RESULT 1</b>							
ID	043655	PRELIMINARY;	PRT;	359 AA.			
AC	043656;						
DT	01-JUN-1998 (TREMBBLE, 06, Last sequence update)						
DT	01-JUN-1998 (TREMBBLE, 06, Last annotation update)						
DE	Hepatitis A virus cellular receptor 1.						
GN	Name=HAVcr-1,						
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TaxID=9606;						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Liver;						
RX	MEDLINE=98:5180; PubMed=9658108;						
RA	Feiglstock D., Thompson P., Mattoo P., Zhang Y., Kaplan G.G.,						
RT	"The human homolog of HAVcr-1 codes for a hepatitis A virus cellular receptor"; DR J. Virol. 72:6621-6628 (1998).						
RU	EMBL; AF043724; AAC39862.1; -.						
<b>RESULT 2</b>							
ID	096D42	PRELIMINARY;	PRT;	364 AA.			
AC	Q96D42;						
DT	01-DEC-2001 (TREMBBLE, 19, Created)						
DT	01-OCT-2004 (TREMBBLE, 19, Last sequence update)						
DE	HAVCR1_protein.						
DN	Name=HAVCR1,						
DR	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
RA	Klauser R.D., Eichner R., Schaeffer C.P., Brat N.R.,						
RA	Atschul S.F., Zeeberg B.R., Buetow K.H., Schaeffer C.P., Brat N.R.,						
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,						
RA	Ditachenko L., Marusina K., Farmer A.A., Rubin R.M., Hong L.,						
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,						
RA	Brownstein M.J., Udin T.B., Tohiyuki S., Carninci P., Prange C.,						
RA	Rana S.S., Loqueilano N.A., Peters G.J., Abramson R.D., Mullikay S.J.,						
RA	Bokas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,						
RA	Richards S., Morley K.C., Hale S., Maruyama A.M., Gay L.J., Hulyk S.W.,						
RA	Villalon D.K., Murzy D.M., Sodergran B.J., Lu X., Gibbo R.A.,						
RA	Faney J., Heiton E., Kettman M., Macan A., Rodrigues S., Sanchez A.,						
RA	Blakesley R.W., Young A.C., Shvchenko K.Y., Bouffard G.G.,						
RA	Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,						
RA	Krzewinski M.I., Skalska U., Smialik D.E., Schnurch A., Scheine J.E.,						
RA	Jones S.J., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human						
RT	and mouse cDNA sequences.," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).						
RL	[2].						
RN	SEQUENCE FROM N.A.						
RC	TISSUE=Kidney/;						
RA	Straubberg R.;						
RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.						
RN	[3].						
RP	SEQUENCE FROM N.A.						
RA	Ebert L., Schick M., Neubert P., Schattner R., Henze S., Korn B.;						
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; BC013325; AARH1335.1; -.						
DR	EMBL; CQ457114; CGG33395.1; -.						
DR	GeneW; HGNC:1786; HAVCR1.						
DR	InterPro; IPR003059; Ig.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003066; Ig_MHC.						
DR	Pram; PF00047; ig; 1.						

DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 364 AA; 39249 MW; AA67CTC7FAC81F1 CRC64;  
 Query Match 100.0%; Score 99; DB 2; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNNNOTQLEHHS 18  
 Db 269 SSDGLWNNNOTQLEHHS 286

RESULT 3  
 CAG33395 PRELIMINARY; PRT; 364 AA.  
 ID CAG33395; PROSITE; PS50835; IG\_LIKE; 1.  
 DT 01-JUN-2004 (TREMBLrel. 27, Created)  
 DT 01-JUN-2004 (TREMBLrel. 27, Last sequence update)  
 DT 01-JUN-2004 (TREMBLrel. 27, Last annotation update)  
 DE HAVER1 protein.  
 GN HAVER1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ebert L., Schick M., Neubert P., Scharffen R., Henze S., Korn B.;  
 RT "Cloning of human full open reading frames in Gateway™ system entry  
 vector (pDON201);"  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CH457114; CAG33395.1; -.  
 SQ SEQUENCE 364 AA; 39249 MW; AA67CTC7FAC81F1 CRC64;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA EMBL; CH457114; CAG33395.1; -.  
 RT "Molecular cloning of the hepatitis A virus receptor from a simian  
 cell line."  
 RL J. Gen. Virol. 78:1565-1569(1997).  
 DR EMBL; DB88585; BA21556.1; -.  
 DR GO; GO:0004872; PReceptor activity; IEA.  
 DR InterPro; IPR01559; IG.  
 RT "Molecular cloning of the hepatitis A virus receptor from a simian  
 cell line."  
 RL J. Gen. Virol. 78:1565-1569(1997).  
 DR EMBL; DB88585; BA21556.1; -.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 460 AA; 49887 MW; ID1A0C1D832139EA CRC64;

RESULT 4  
 Q95144 PRELIMINARY; PRT; 451 AA.  
 ID Q95144; PROSITE; PS50835; IG\_LIKE; 1.  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE HAVER1 protein precursor.

OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 TISSUE=Kidney;  
 RX MEDLINE:97015129; PubMed=8861957;  
 RA Kaplan G., Tobeoka A., Thompson P., Akatsuwa T., Moritsugu Y.,  
 RA Feinstein S.M.;  
 RT "Identification of a surface glycoprotein on African green monkey  
 kidney cells as a receptor for hepatitis A virus";  
 RL IMBO J. 15:222-4296(1996).  
 DR PIR; S71754; S71754;  
 DR InterPro; IPR00599; IG.  
 DR InterPro; IPR00710; Ig-like.  
 DR SMART; SM00409; IG; 1.

PROSITE; PS50835; IG\_LIKE; 1.  
 PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Signal.;  
 FT SIGNAL.;  
 SQ SEQUENCE 451 AA; 48774 MW; 5D3955455AA4332 CRC64;  
 Query Match 84.8%; Score 84; DB 2; Length 451;  
 Best Local Similarity 88.9%; Pred. No. 9.5e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNNNOTQLEHHS 18  
 Db 344 SSDGLWNNNOTQLEHHS 361

RESULT 5  
 O18984 PRELIMINARY; PRT; 460 AA.  
 ID O18984; PROSITE; PS50835; IG\_LIKE; 1.  
 AC 018984;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hepatitis A virus receptor.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97368416; PubMed=9225030;  
 RA Ashida M., Hamada C.;  
 RT "Molecular cloning of the hepatitis A virus receptor from a simian  
 cell line."  
 RL InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 460 AA; 49887 MW; ID1A0C1D832139EA CRC64;

Query Match 84.8%; Score 84; DB 2; Length 460;  
 Best Local Similarity 88.9%; Pred. No. 9.7e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNNNOTQLEHHS 18  
 Db 353 SSDGLWNNNOTQLEHHS 370

RESULT 6  
 O7UJ48 PRELIMINARY; PRT; 469 AA.  
 ID O7UJ48; PROSITE; PS50835; IG\_LIKE; 1.  
 AC O7UJ48; PROSITE; PS50835; IG\_LIKE; 1.  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hepatitis A virus cellular receptor 1 short form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TAXID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98285791; PubMed=6921093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;

RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 RL EMBL; ARF43446; AAC39711.; -.  
 DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; Ig-like.  
 DR InterPro; IPR00110; Ig-like.  
 DR InterPro; IPR00306; Ig\_MHC.  
 DR SMART; SMO409; Ig; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW Receptor; PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE: 469 AA; 50561 MW; 278386F47948F528 CRC64;  
 Query Match 84.8%; Score 84; DB 2; Length 469;  
 Best Local Similarity 88.9%; Pred. No. 9.9e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 362 SSDGLWNNTQTLFLEHS 379

RESULT 7

ID Q7UJ47 PRELIMINARY; PRT; 473 AA.  
 RP SEQUENCE FROM N.A.  
 AC Q7UJ47; PubMed=9621093;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Hepatitis A virus cellular receptor 1 short form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98285791; PubMed=9621093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;  
 RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 DR EMBL; ARF43448; AAC39731.; -.  
 DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; Ig-like.  
 DR InterPro; IPR00110; Ig-like.  
 DR SMART; SMO409; Ig; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW Receptor; PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE: 474 AA; 51088 MW; 472DF87C9220524 CRC64;  
 Query Match 84.8%; Score 84; DB 2; Length 474;  
 Best Local Similarity 88.9%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 367 SSDGLWNNTQTLFLEHS 384

RESULT 9

ID Q46598 PRELIMINARY; PRT; 478 AA.  
 RP SEQUENCE FROM N.A.  
 AC Q46598; PRELIMINARY;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DE Hepatitis A virus cellular receptor 1 long form.  
 GN Name=HAVER-1;  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98285791; PubMed=9621093;  
 RA Feigelson D., Thompson P., Mattoo P., Kaplan G.G.;  
 RT "Polymorphisms of the hepatitis A virus cellular receptor 1 in African green monkey kidney cells result in antigenic variants that do not react with protective monoclonal antibody 190/4.";  
 RT J. Virol. 72:6218-6222(1998).  
 DR EMBL; ARF43449; AAC39774; -.  
 DR GO; GO:0004872; F-receptor activity; IEA.  
 DR InterPro; IPR03599; Ig-like.  
 DR InterPro; IPR00110; Ig-like.  
 DR SMART; SMO409; Ig; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW Receptor; PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE: 478 AA; 51501 MW; 3A919655C752FF60 CRC64;  
 Query Match 84.8%; Score 84; DB 2; Length 478;  
 Best Local Similarity 88.9%; Pred. No. 0.0001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQTLFLEHS 18  
 Db 366 SSDGLWNNTQTLFLEHS 383

RESULT 8

ID Q46597 PRELIMINARY; PRT; 474 AA.  
 RP SEQUENCE FROM N.A.  
 AC Q46597; PRELIMINARY;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

**Db** 371 | ||| SDGLWNNTQQLSPERHS 388  
**CEMA\_NEPOL**, STANDARD; PRT; 392 AA.  
**ID** Q9TKE2; [1]  
**DT** 16-OCT-2001 (Rel. 40, Created)  
**DT** 16-OCT-2001 (Rel. 40, Last sequence update)  
**DT** 05-JUL-2004 (Rel. 44, Last annotation update)  
**DE** Chloroplast envelope membrane protein.  
**GN** Name=cema;  
**OS** Nephroselmis olivacea.  
**OC** Chloroplast; Viridiplantae; Chlorophyta; Prasinophyceae;  
**OC** Chlorodendratales; Chlorodendraceae; Nephroselmis.  
**RN** NCBI\_TAXID=31312; [1]  
**RP** SEQUENCE FROM N.A.  
**RC** STRAIN=NIES-484;  
**RX** MEDLINE=99398694; PubMed=10468594;  
**RA** Turnel M., Otis C., Lemieux C.; sequence of the green alga *Nephroselmis* olivacea: insights into the architecture of ancestral chloroplast genomes.;  
**RT** Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999). Indirectly promotes efficient inorganic carbon uptake into chloroplasts (By similarity).  
**CC** -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast inner envelope (By similarity).  
**CC** -!- SIMILARITY: Belongs to the cema family.  
**CC** This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
**CC** EMBL; AF137379; AAD54824.1; -. DR HAMAP; MF\_01308; ; 1.  
**DR** InterPro; IPR04282; Cema.  
**DR** Pfam; PF03040; Cema; 1.  
**KW** Chloroplast; Hydrogen ion transport; Transmembrane; Transport.  
**FT** TRANSMEM 172 194 Potential.  
**FT** TRANSMEM 267 289 Potential.  
**FT** TRANSMEM 315 337 Potential.  
**FT** TRANSMEM 352 373 Potential.  
**SQ** SEQUENCE ' 392 AA, 45537 MW; DRCB7A56FEE88E8 CRC64;

**Query Match** 51.5%; Score 51; DB 1; length 392; Best Local Similarity 69.2%; Pred. No. 14; Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

**RESULT 11**

**OY** 6 WNNNOTOLEHRS 18  
**Db** 202 WNNNOTOLEHRS 214

**RESULT 11**

**OY** 6 WNNNOTOLEHRS 18  
**Db** 202 WNNNOTOLEHRS 214

**CEMA\_GUTH**, STANDARD; PRT; 278 AA.  
**ID** CEMA\_GUTH 078470; [1]  
**DT** 15-DEC-1998 (Rel. 37, Created)  
**DT** 05-JUL-2004 (Rel. 44, Last sequence update)  
**DE** Chloroplast envelope membrane protein.  
**GN** Name=cema; Synonyms=ycf1.0;  
**OS** Guillardia theta (Cryptomonas phi).  
**OC** Chloroplast; Cryptophyta; Cryptomonadaceae; Guillardia.  
**OX** NCBI\_TAXID=55529; [1]  
**RP** SEQUENCE FROM N.A.  
**RC** MEDLINE=99128721; PubMed=9929392;  
**RA** Douglas S.E., Penny S.L.; the plastid genome of the cryptophyte alga, *Guillardia theta*: complete sequence and conserved synteny groups confirm its common ancestry with red algae.;  
**RT** J. Mol. Evol. 48:236-244(1999).  
**CC** -!- FUNCTION: May be involved in proton extrusion. Indirectly promotes efficient inorganic carbon uptake into chloroplasts (By similarity).  
**CC** -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast inner envelope (By similarity).  
**CC** -!- SIMILARITY: Belongs to the cema family.  
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**CC** EMBL; AF041468; AAC35661.1; -. DR HAMAP; MF\_01308; ; 1.  
**DR** InterPro; IPR04282; Cema.  
**DR** Pfam; PF03040; Cema; 1.  
**KW** Chloroplast; Hydrogen ion transport; Transmembrane; Transport.  
**FT** TRANSMEM 60 80 Potential.  
**FT** TRANSMEM 163 183 Potential.

**OG** Anabaena sp. (strain PCC 7120).  
**OS** Plasmid pCC7120beta.





DR GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR00936; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR InterPro; IPR000336; Flavi\_glycoprote.

DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.

DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.

DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.

KW Polyprotein.

FT NON\_TER 1 1

FT CHAIN <1 537 envelope glycoprotein E2.

FT CHAIN 538 558 AA; 61626 MW; 95ED71BDDF81B58C CRC64;

SQ SEQUENCE 558 AA; 558

Query Match 48.5%; Score 48; DB 2; Length 558;

Best Local Similarity 50.0%; Pred. No. 61;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNWNQOMFWIQ 502

RESULT 18

ID 036297 PRELIMINARY; PRT; 559 AA.

AC 036297;

DT 01-JAN-1998 (TREMBREL. 05, Created)

DT 01-JAN-1998 (TREMBREL. 05, Last sequence update)

DB 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Polyprotein (Fragment).

DR Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.; "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus."; J. Virol. 71:6697-6705(1997).

DR EMLI; AR00469; AB81714.1; -.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000336; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.

DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.

DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.

KW Polyprotein.

FT NON\_TER 1 1

FT CHAIN <1 537 envelope glycoprotein E2.

FT CHAIN 538 559 AA; 61749 MW; 93A484BFCA29217P CRC64;

SQ SEQUENCE 559 AA; 559

Query Match 48.5%; Score 48; DB 2; Length 559;

Best Local Similarity 57.9%; Pred. No. 61;

Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Db 487 SLDHLWNWNQOMFWIQ 505

RESULT 20

ID 036308 PRELIMINARY; PRT; 559 AA.

AC 036308;

DT 01-JAN-1998 (TREMBREL. 05, Created)

DT 01-JAN-1998 (TREMBREL. 05, Last sequence update)

DB 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE Polyprotein (Fragment).

DR Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.; "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus."; J. Virol. 71:6697-6705(1997).

DR EMLI; AR00469; AB81715.1; -.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

Query Match 48.5%; Score 48; DB 2; Length 559;

Best Local Similarity 50.0%; Pred. No. 61;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNWNQOMFWIQ 502

RESULT 19

RP STRAIN=9001;

RX MEDLINE=97405681; PubMed=9261393;

RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;

RT "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.";

OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; OC Alphavirus; VEEV complex.

OX NCBI\_TaxID=11036;

[1]

RN SEQUENCE FROM N.A.

RP

RC

RA

RA

RT

RT

DB

OC

OC

OX

GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR InterPro; IPR000336; Flavi\_glycoprote.

DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.

DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.

DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.

KW Polyprotein.

FT NON\_TER 1 1

FT CHAIN <1 537 envelope glycoprotein E2.

FT CHAIN 538 559 AA; 61837 MW; 2C273D694EDFB64D CRC64;

SQ SEQUENCE 559 AA; 559

Query Match 48.5%; Score 48; DB 2; Length 559;

Best Local Similarity 50.0%; Pred. No. 61;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNWNQOMFWIQ 502

RP STRAIN=DBT5191;

RX MEDLINE=97405681; PubMed=9261393;

RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M., Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;

RT "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.";

OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; OC Alphavirus; VEEV complex.

OX NCBI\_TaxID=11036;

[1]

RP

RC

RA

RA

RT

RT

DB

OC

OC

OX

GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.  
 FT NON TER 1 1 envelope glycoprotein E2.  
 FT CHAIN <1 537 envelope glycoprotein E1.  
 FT CHAIN 538 >559  
 FT NON TER 559 559 MW: AF95E1323F72337 CRC64;  
 SEQUENCE 559 AA: 61784 MW:  
 Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 OQ 1 SSDGLWNNNNOTQLELE 16  
 Db 487 SLDHLWNNNQQMFWMQ 502

RESULT 21

ID 036309 PRELIMINARY; PRT; 559 AA.

AC 036309;  
 DT 01-JAN-1998 (TREMBUREL. 05, Created)  
 DT 01-JAN-1998 (TREMBUREL. 05, Last sequence update)  
 DT 01-OCT-2003 (TREMBUREL. 25, Last annotation update)

DB Polyprotein (fragment).

OS Venezuelan equine encephalitis virus.  
 OC viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.

RA NCBI\_TaxID=11036;

RN [1]

RP STRAIN=Panaquire;

RC Weaver S.C.;  
 RA Submitted (SERP-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; U5346; AAC2613.1; --

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:005198; P:structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR InterPro; IPR002548; Alpha\_E1\_glycop.

DR InterPro; IPR000936; Alpha\_E2\_glycop.

DR InterPro; IPR002533; Alpha\_E3\_glycop.

DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 1 1 protein E2.  
 FT CHAIN <1 537 protein E1.  
 FT NON TER 538 >559  
 SEQUENCE 559 AA: 61754 MW: C48D0AE23677E6A0 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OQ 1 SSDGLWNNNNOTQLELE 16  
 Db 487 SLDHLWNNNQQMFWMQ 502

RESULT 23

ID Q9WC9 PRELIMINARY; PRT; 559 AA.

AC Q9WC9;  
 DT 01-NOV-1999 (TREMBUREL. 12, Created)  
 DT 01-NOV-1999 (TREMBUREL. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBUREL. 25, Last annotation update)

DB Structural polyprotein (Fragment).

OS Venezuelan equine encephalitis virus.  
 OC viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.

RA NCBI\_TaxID=11036;

RN [1]

RP STRAIN=Pura;

RC Weaver S.C.; Pfeiffer M.; Marriott K.; Kang W.; Kinney R.M.;  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis  
 virus subtype TAB outbreaks"; Am. J. Trop. Med. Hyg. 60:441-448 (1999).  
 DR EMBL; AF093104; AAD37003.1; --  
 DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

RESULT 22

ID 041997 PRELIMINARY; PRT; 559 AA.

DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E2\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 52045 MW; 66469E1C6BB17B50 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNNGNQMFWIQ 502

RESULT 24

Q9WCG0 PRELIMINARY; PRT; 559 AA.  
 AC Q9WCG0;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Structural polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 RT viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 RN [1] \_TAXID=11036;

RC SEQUENCE FROM N.A.

DR EMBL; AR093105; Aad370041; -.  
 DR GO; GO:0019028; C-viral capsid; IEA.  
 DR GO; GO:0019031; C-viral envelope; IEA.  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis  
 virus subtype LAB outbreaks";  
 RL Am. J. Trop. Med. Hyg. 60:441-448(1999).

RX MEDLINE-99394886; PubMed=10466974;  
 RA Weaver S.C., Prefeer M., Marriott K., Kang W., Kinney R.M.;  
 RT "Genetic evidence for the origins of Venezuelan equine encephalitis  
 virus subtype LAB outbreaks";  
 RL Am. J. Trop. Med. Hyg. 60:441-448(1999).

DR EMBL; AR093105; Aad370041; -.  
 DR GO; GO:0019028; C-viral capsid; IEA.  
 DR GO; GO:0005198; F-structural molecule activity; IEA.

DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR002536; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF000943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 61822 MW; E03AD37D4AB6AB54 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNNGNQMFWIQ 502

RESULT 25

Q98755 PRELIMINARY; PRT; 559 AA.  
 ID Q98755  
 AC 098755;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

RA Weaver S.C., Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RL Weaver S.C., Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AR348316; Aad57189.1; -.  
 DR GO; GO:0019028; C-viral capsid; IEA.  
 DR GO; GO:0019031; C-viral envelope; IEA.  
 DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000936; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 61823 MW; 9D14BF8740780862 CRC64;

DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E2\_glycop.  
 DR InterPro; IPR00936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 52045 MW; 66469E1C6BB17B50 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNNGNQMFWIQ 502

RESULT 26

Q8V5J7 PRELIMINARY; PRT; 559 AA.  
 ID Q8V5J7  
 AC Q8V5J7;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Structural polyprotein (Fragment).  
 OS Venezuelan equine encephalitis virus.  
 RT viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 RN [1] \_TAXID=11036;

RC SEQUENCE FROM N.A.

DR Weaver S.C., Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RL Weaver S.C., Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AR348316; Aad57189.1; -.  
 DR GO; GO:0019028; C-viral capsid; IEA.  
 DR GO; GO:0019031; C-viral envelope; IEA.  
 DR GO; GO:0005198; F-structural molecule activity; IEA.  
 DR InterPro; IPR002548; Alpha\_E1\_glycop.  
 DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR000936; Flavi\_glycoprote.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 KW Polyprotein.

FT NON TER 559 559  
 SQ SEQUENCE 559 AA; 61822 MW; E03AD37D4AB6AB54 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 559;  
 Best Local Similarity 50.0%; Pred. No. 61;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 487 SLDHLWNNGNQMFWIQ 502





FT TRANSMEM 792 808 Potential.  
 FT TRANSMEM 1231 1247 Potential.  
 FT CARBOHYD 286 N-linked (GLCNAC. . .) (Potential).  
 FT CARBOHYD 546 546 N-linked (GLCNAC. . .) (Potential).  
 FT CARBOHYD 652 652 N-linked (GLCNAC. . .) (Potential).  
 FT CARBOHYD 946 946 N-linked (GLCNAC. . .) (Potential).  
 FT CONFLICT 811 811 P -> G (in Ref. 2).  
 SQ SEQUENCE 1254 AA; 138390 MW; 1C0F62BE1909664B CRC64;

Query Match 48.5%; Score 48; DB 1; Length 1254;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02; 3; Mismatches 5; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SDGIGANNNOTQFLIE 16  
 Db 763 SLDHLWNNNQQMFWIQL 778

RESULT 31

077VY8 PRELIMINARY; PRT; 1254 AA.

ID 077VY8 PRELIMINARY; PRT; 1254 AA.

AC 077VY8; 5 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DB Structural polyprotein.

OS Venezuelan equine encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;

OC Alphavirus; VEEV complex.

OC Alphavirus; VEEV complex.

OX NCBI\_TaxID=11036;

RN [1];

RP SEQUENCE FROM N.A.

RC STRAIN=Cabasou\_Car 508;

RX MEDLINE=99101297; PubMed=9886206;

RA Kinney R.M., Pfeiffer M., Tsuchiya K.R., Chang G.J., Roehrig J.T.;  
 "Nucleotide sequences of the 26S mRNAs of the viruses defining the  
 Venezuelan equine encephalitis antigenic complex.";  
 Am. J. Trop. Med. Hyg. 59:952-964(1998).

RL EMBL; AR075251; ADI14551.1; -.

DR InterPro; IPR002533; Alpha\_E1\_glycop.

DR InterPro; IPR002536; Alpha\_E2\_glycop.

DR InterPro; IPR002537; Alpha\_B3\_glycop.

DR InterPro; IPR002538; Flavi\_glycoprote.

DR InterPro; IPR000930; Peptidase\_S3.

DR InterPro; IPR009033; Pept\_Ser\_Cys.

DR Pfam; PF00944; Alpha\_core\_1.

DR Pfam; PF00943; Alpha\_E1\_glycop; 1.

DR Pfam; PF01563; Alpha\_E2\_glycop; 1.

DR Prints; PR00798; TOGAVIRIN.

KW Polyprotein.

FT CHAIN 813 1254 envelope glycoprotein 1.

FT CHAIN 1 274 nucleocapsid protein.

FT CHAIN 275 333 polyprotein cleavage product E3.

FT CHAIN 334 756 envelope glycoprotein 2.

FT CHAIN 757 812 6K polyprotein cleavage product.

SQ SEQUENCE 1254 AA; 138337 MW; 29DD8R37F8E92CAB CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1254;  
 Best Local Similarity 57.9%; Pred. No. 1.5e+02; 3; Mismatches 4; Indels 4; Gaps 1;  
 Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

OY 1 SDGIGANNNOTQFLIE 15  
 Db 762 SLDHLWNNNQQMFWIQL 780

RESULT 33

ADI4551 PRELIMINARY; PRT; 1254 AA.

ID ADI4551 PRELIMINARY; PRT; 1254 AA.

AC ADI4551; 5 (TREMBLrel. 27, Created)

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)

DB Structural polyprotein.

OS Venezuelan equine encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;

OC Alphavirus.

OX NCBI\_TaxID=11036;

RP SEQUENCE FROM N.A.

RC STRAIN=Everglade\_Fe3-7c;

RX MEDLINE=99101297; PubMed=9886206;

RA Kinney R.M., Pfeiffer M., Tsuchiya K.R., Chang G.J., Roehrig J.T.;  
 "Nucleotide Sequences of the 26S mRNAs of the viruses defining the  
 Venezuelan equine encephalitis antigenic complex.";  
 Am. J. Trop. Med. Hyg. 59:952-964(1998).

RL EMBL; AR075251; ADI14551.1; -.

DR HSSP; P05674; IEPs.

DR GO; GO:0016020; C\_membrane; IEA.

DR GO; GO:0019028; C\_viral\_capsid; IEA.

DR GO; GO:0004228; F\_serine-type\_endopeptidase\_activity; IEA.

DR GO; GO:0005198; P\_structural\_molecule\_activity; IEA.

DR GO; GO:0006508; P\_proteolysis\_and\_peptidolysis; IEA.

DR InterPro; IPR00248; Alpha\_E1\_glycop.

DR InterPro; IPR002533; Alpha\_B3\_glycop.

DR InterPro; IPR002536; Flavi\_glycoprote.

DR InterPro; IPR002537; Alpha\_E2\_glycop.

DR InterPro; IPR000930; Peptidase\_S3.

DR InterPro; IPR009033; Pept\_Ser\_Cys.

DR Pfam; PF00944; Alpha\_core\_1.

DR Pfam; PF00943; Alpha\_E1\_glycop; 1.

DR Pfam; PF01563; Alpha\_E2\_glycop; 1.

DR Prints; PR00798; TOGAVIRIN.

KW Polyprotein.

FT CHAIN 813 1254 envelope glycoprotein 1.

FT CHAIN 1 274 nucleocapsid protein.

FT CHAIN 275 334 polyprotein cleavage product E3.

FT CHAIN 335 756 envelope glycoprotein 2.

FT CHAIN 757 812 6K polyprotein cleavage Product.

SQ SEQUENCE 1254 AA; 138639 MW; 3ED5B5AB788CPB CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1254;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02; 3; Mismatches 4; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 DGLIANNNOTQFLIE 16  
 Db 764 DHLWNNNQQMFWIQL 777



PT	CHAIN	1	275	Coat protein C.	DR	InterPro; IPRO02533; Alpha_E3_glycop.
PT	CHAIN	276	334	Spike glycoprotein E3.	DR	InterPro; IPRO00336; Flavi_glycoprote.
PT	CHAIN	335	757	Spike glycoprotein E2.	DR	InterPro; IPRO0030; Peptidase_S3.
PT	CHAIN	758	813	6 kDa peptide.	DR	InterPro; IPRO09003; Pept_Ser_Cys.
PT	ACT_SITE	814	1255	Spike glycoprotein E1.	DR	Pfam; PF00944; Alpha core; 1.
PT	ACT_SITE	152	158	(By similarity).	DR	Pfam; PF01589; Alpha_E1_glycop; 1.
PT	ACT_SITE	226	226	Charge relay system (By similarity).	DR	Pfam; PF00943; Alpha_E2_glycop; 1.
PT	TRANSMEM	702	722	Charge relay system (By similarity).	DR	Pfam; PF01563; Alpha_E3_glycop; 1.
PT	TRANSMEM	795	814	Potential.	DR	PRINS; PR00798; TOGAVIRIN.
PT	TRANSMEM	1232	1249	Potential.	DR	Polyprotein.
PT	CARBOHYD	47	N-linked (GLCNAC. . .) (Potential).	DR	SEQUENCE 1255 AA; 138213 MW; 33CD302F5CAB8646 CRC64;	
PT	CARBOHYD	286	N-linked (GLCNAC. . .) (Potential).	DR	Query Match 48.5%; Score 48; DB 1; Length 1255;	
PT	CARBOHYD	652	N-linked (GLCNAC. . .) (Potential).	DR	Best Local Similarity 50.0%; Pred. No. 1.5e+02;	
PT	CARBOHYD	947	N-linked (GLCNAC. . .) (Potential).	DR	Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	
SQ	SEQUENCE	1255 AA;	138213 MW;	33CD302F5CAB8646 CRC64;	DR	SEQUENCE 1255 AA; 138339 MW; 799350E33C807EAA CRC64;
Qy	1	SSDGHLWNNOOTQFLLE 16	SLDHWNWNQOMFWIQ 778	Db	763 SLDHWNWNQOMFWIQ 778	
RESULT 36				Db	763 SLDHWNWNQOMFWIQ 778	
ID	036287	PRELIMINARY;	PRT; 1255 AA.	Qy	1 SSDGHLWNNOOTQFLLE 16	
AC	036287:	036301;	036288	PRELIMINARY;	PRT; 1255 AA.	
DT	01-JAN-1998	(TREMBLel. 05, Created)	036288;	PRELIMINARY;	PRT; 1255 AA.	
DT	01-NOV-1999	(TREMBLel. 12, Last sequence update)	036288;	PRELIMINARY;	PRT; 1255 AA.	
DT	05-JUL-2004	(TREMBLel. 27, Last annotation update)	036288;	PRELIMINARY;	PRT; 1255 AA.	
DE	Structural polyprotein.	Venezuelan equine encephalitis virus.	036288;	PRELIMINARY;	PRT; 1255 AA.	
OS	Venezuelan equine encephalitis virus.	Venezuelan equine encephalitis virus.	036288;	PRELIMINARY;	PRT; 1255 AA.	
OC	OC	OC	036288;	PRELIMINARY;	PRT; 1255 AA.	
OX	NCBI_TaxID=1036;	Alpha virus; VEEV complex.	036288;	PRELIMINARY;	PRT; 1255 AA.	
RN	[1]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RX			036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,	036288;	PRELIMINARY;	PRT; 1255 AA.		
RA	Smith J.F., Kang W., Sweeney W.P., Weaver S.C.;	036288;	PRELIMINARY;	PRT; 1255 AA.		
RT	"Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.";	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	J. Virol. 71:6697-6705(1997).	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[2]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RX	MEDLINE=99214366; PubMed=10196323;	036288;	PRELIMINARY;	PRT; 1255 AA.		
RA	Wang E., Barrera R., Ferro C., Freier J.E., Navarro J.C.,	036288;	PRELIMINARY;	PRT; 1255 AA.		
RA	Sala R., Vasquez C., Weaver S.C.,	036288;	PRELIMINARY;	PRT; 1255 AA.		
RT	"Genetic and phenotypic changes accompanying the emergence of epizootic subtype IC Venezuelan equine encephalitis viruses from an enzootic subtype ID progenitor.";	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	J. Virol. 73:4266-4271(1999).	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	036288;	PRELIMINARY;	PRT; 1255 AA.		
RN	[3]		036288;	PRELIMINARY;	PRT; 1255 AA.	
RP	SEQUENCE FROM N.A.		036288;	PRELIMINARY;	PRT; 1255 AA.	
RC	STRAIN=6637, and 66457;		036288;	PRELIMINARY;	PRT; 1255 AA.	
RA	Wang E., Weaver S.C., to					

DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PRO1563; Alpha\_E2\_glycop; 1.  
 DR PRINTS; PR00798; TOGAVIRIN.  
 KW Polyprotein.

SEQUENCE 1255 AA; 138564 MW; 9229511B3907A399 CRC64;

Qy 1 SSDGIWNNNQTMFVHQ 16  
 Db 763 SLDHLWNNNQQMFWIQ 778

RESULT 38  
 ID 036300 PRELIMINARY; PRT; 1255 AA.  
 AC 036300;  
 DT 01-JAN-1998 (TREMBREL 05, Created)  
 DT 01-MAY-1999 (TREMBREL 10, Last sequence update)  
 DT 01-MAR-2004 (TREMBREL 26, Last annotation update)  
 DE Structural polyprotein.  
 GN Name=ns14;  
 OS Venezuelan equine encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 OX NCBI\_TaxID=11036;  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=Beck/Wycoff,  
 RX MEDLINE-97404681; PubMed=9251393;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.P., Kang W., Sweeney W.P., Weaver S.C.;  
 RT "Repeated emergence of epidemic/epizootic Venezuelan equine encephalitis from a single genotype of enzootic subtype ID virus.",  
 RT J. Virol. 71:6697-6705(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Beck/Wycoff;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.P., Kang W., Sweeney W.P., Weaver S.C.;  
 RA Submitted (SERB-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF044471; AAC36374.1; -.  
 DR HSSP; P05674; IEP5.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0004222; F:serine-type endopeptidase activity; IEA.  
 DR GO; GO:000330; F:structural molecule activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR002248; Alpha\_E1\_glycop.  
 DR InterPro; IPR000336; Alpha\_E2\_glycop.  
 DR InterPro; IPR002333; Alpha\_B3\_glycop.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR InterPro; IPR000330; Peptidase\_S3.  
 DR InterPro; IPR00903; Pept\_Ser\_Cys.  
 DR Pfam; PRO0944; Alpha\_core; 1.  
 DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.  
 DR PRINTS; PR00798; TOGAVIRIN.  
 FT CHAIN 538 1255 envelope glycoprotein E1.  
 FT CHAIN 1 537 envelope glycoprotein E2.  
 SQ SEQUENCE 1255 AA; 138476 MW; 2CIECB6F196BC751 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1255;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 SSDGIWNNNQTMFVHQ 16  
 Db 763 SLDHLWNNNQQMFWIQ 778

RESULT 39  
 ID 090164 PRELIMINARY; PRT; 1255 AA.  
 AC 090164;  
 DT 01-NOV-1998 (TREMBREL 08, Created)  
 DT 01-NOV-1998 (TREMBREL 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBREL 26, Last annotation update)  
 DE Structural polyprotein.  
 OS Venezuelan equine encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 OX NCBI\_TaxID=11036;  
 RN [1]  
 RP STRAIN=71-180;  
 RX MEDLINE-89243175; PubMed=2524126;  
 RA Kinney R.M., Johnson B.J., Welch J.B., Tsuchiya K.R., Trent D.W.;  
 RT "The full-length nucleotide sequences of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and its attenuated vaccine derivative, strain TC-83.",  
 RT Virology 170:19-30(1989).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=71-180;  
 RX MEDLINE-93107872; PubMed=1469368;  
 RA Kinney R.M., Tsuchiya K.R., Sneider J.M., Trent D.W.;  
 RT "Molecular evidence for the origin of the widespread Venezuelan equine encephalitis epidemic of 1969 to 1972.",  
 RT J. Gen. Virol. 73:0-0(0).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=71-180;  
 RA Kinney R.M., Trent D.W.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF069903; AAC24034.1; -.  
 DR HSSP; P05674; IEP5.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPK00036; Alpha\_E1\_glycop.  
 DR InterPro; IPR000336; Alpha\_E2\_glycop.  
 DR InterPro; IPR002333; Alpha\_B3\_glycop.  
 DR InterPro; IPK00036; Flavi\_glycoprote.  
 DR InterPro; IPR000330; Peptidase\_S3.  
 DR InterPro; IPR00903; Pept\_Ser\_Cys.  
 DR Pfam; PRO0944; Alpha\_core; 1.  
 DR Pfam; PRO1589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PRO0943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PRO1563; Alpha\_E3\_glycop; 1.  
 DR PRINTS; PR00798; TOGAVIRIN.  
 KW Polyprotein.

FT CHAIN 814 1255 E1.  
 FT CHAIN 276 334 capsid protein.  
 FT CHAIN 335 757 E2.  
 FT CHAIN 758 813 6K polypeptide.

SQ SEQUENCE 1255 AA; 138458 MW; 8A73DC7501404C2 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1255;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SSDGIWNNNQTMFVHQ 16  
 Db 763 SLDHLWNNNQQMFWIQ 778

RESULT 40  
 091628 PRELIMINARY; PRT; 1255 AA.  
 ID 091628;  
 AC 091628;  
 DT 01-NOV-1998 (TREMBrel. 08, Created)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DE Structural polyprotein.  
 GN Name=n84;  
 OS Venezuelan equine encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus; VEEV complex.  
 OX NCBI\_TaxID=11036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=6921;  
 RX MEDLINE=9740681; PubMed=9261393;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.P., Kang W., Sweeney W.P., Weaver S.C.;  
 RT "Repeated emergence of epidemic/epizootic Venezuelan equine  
 encephalitis from a single genotype of enzootic subtype ID virus.";  
 RL J. Virol. 71:6697-6705(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=921;  
 RA Powers A.M., Oberste M.S., Brault A.C., Rico-Hesse R., Schmura S.M.,  
 RA Smith J.P., Kang W., Sweeney W.P., Weaver S.C.;  
 RL Submitted (SSB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AR0004470; AAC36375.1; -  
 DR HSPB; P05674; IEP5;  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0019028; C-viral capsid; IEA.  
 DR GO; GO:0019031; C-viral envelope; IEA.  
 DR GO; GO:0004232; Fibserine-type endopeptidase activity; IEA.  
 DR GO; GO:0005138; F-structural molecule activity; IEA.  
 DR GO; GO:0006508; Peptidase and peptidolysis; IEA.  
 DR InterPro; IPR002540; Alpha\_E1\_glycop.  
 DR InterPro; IPR000936; Alpha\_E2\_glycop.  
 DR InterPro; IPR002533; Alpha\_E3\_glycop.  
 DR InterPro; IPR003336; Flavi\_glycoprote.  
 DR InterPro; IPR000930; Peptidase\_S3.  
 DR InterPro; IPR00903; Pept\_Ser\_CYB.  
 DR Pfam; PF00944; Alpha\_core; 1.  
 DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
 DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
 DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
 DR PRIMIS; PR00798; TOGA VIRIN.  
 KW Polyprotein.  
 FT CHAIN 538 1255 envelope glycoprotein E1.  
 FT CHAIN 1 537 envelope glycoprotein E2.  
 SQ SEQUENCE 1255 AA; 138365 MW; F08FA923B9C0BA2 CRC64;

Query Match 48.5%; Score 48; DB 2; Length 1255;  
 Best local similarity 50.0%; Pred. No. 1.5e-02;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 SSDGLWNNTQFLR 16  
 Db 763 SLDHHLWNNNQQMFWIQ 778

Search completed: December 30, 2004, 16:13:13  
 Job time : 196 secs

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Gencore version 5.1.6

Run on: December 30, 2004, 15:55:44 ; Search time 154 Seconds  
 (without alignments)  
 41.929 Million cell updates/sec

### Om protein - protein search, using sw model

Title:	US-10-718-321-1					
Perfect score:	99					
Sequence:	1 SSDGLIANNNQTLFLEHS 18					
Scoring table:	BLOSUM62					
	Gapop 10.0 , Gapext 0.5					
Searched:	2002273 seqs, 358729299 residues					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 150 summaries					
Database :	A_Geneseq_23Sep04:*					
	1: geneseq1980s:*					
	2: geneseq1990s:*					
	3: geneseq2000s:*					
	4: geneseq2001s:*					
	5: geneseq2002s:*					
	6: geneseq2003s:*					
	7: geneseq2004s:*					
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
Result No.	Score	Query	%	Match Length	DB ID	Description
						SUMMARIES
1	99	100.0	18	6	AA026687	Aac26687 Human KIM
2	99	100.0	18	6	AA026673	Aac26673 Monoclonal
3	99	100.0	81	6	ABP26678	Abp26678 Human KIM
4	99	100.0	263	7	ADE36629	Ade36629 Human Nov
5	99	100.0	263	7	ADE36622	Ade36622 Plasmid
6	99	100.0	263	7	ADE35996	Ade35996 Human Nov
7	99	100.0	334	2	AAW3336	Aaw3336 Human kid
8	99	100.0	334	6	ABP26679	Abp26679 Human KIM
9	99	100.0	339	7	ADP36592	Adp36592 Human Nov
10	99	100.0	339	7	ABP5582	Abp5582 Human can
11	99	100.0	359	6	ABP70439	Abp70439 Amino aci
12	99	100.0	359	6	ABP70438	Abp70438 Amino aci
13	99	100.0	359	6	ABP70440	Abp70440 Amino aci
14	99	100.0	359	6	ABR48174	Abr48174 Human bla
15	99	100.0	359	6	AAO26680	Aao26680 KIM-1 rel
16	99	100.0	359	7	ADE36594	Ade36594 Human Nov
17	99	100.0	359	7	ADN35984	Adn35984 Cancer/can
18	99	100.0	364	6	ABP70443	Abp70443 Amino aci
19	99	100.0	364	6	ABP70442	Abp70442 Amino aci
20	99	100.0	365	6	ABP70440	Abp70440 Amino aci
21	94	94.9	359	6	ABP70441	Abp70441 Amino aci
22	84	84.8	451	2	ABP92803	Abp92803 Hepatitis
23	53	53.5	18	6	AAQ26686	Aaq26686 Human KIM
24	48.5	48.5	981	5	AAB13306	Aab13306 Venezuela
25	46.5	46.5	6	AAQ26688	Aaq26688 Human KIM	

Abg93049 S. cerevi  
 Abp52836 Protein s  
 Adk62270 Disease t  
 Abg71366 Potato pl  
 Adf49214 Oil-absoc  
 Abx7094 MLHR comp  
 Abx7095 MLHR comp  
 Aam2107 Human pol  
 Aam2108 Human pol  
 Aay99671 Human GTP  
 Adg6355 Rat Prote  
 Ade3357 Rat Prote  
 Abp2470 Human pro  
 Abp97591 Novel hum  
 Aar4192 Rat NMDA  
 Aar42054 Glutamic  
 Aar7126 Human NR2  
 Abb57341 Human GTP  
 Abc7242 Rat ionot  
 Adr49193 Rat ionot  
 Abz9445 Protein e  
 Abz9446 Protein e  
 Ado29254 Mouse GPC  
 Aap96204 Human mus  
 Aam3244 Human pol  
 Aae01972 Human cho  
 Aae01970 Human cho  
 Aae01971 Human cho  
 Aae01973 Human cho  
 Aae01974 Human cho  
 Aae01975 Human cho  
 Aae01976 Human cho  
 Aae01977 Human cho  
 Aae01978 Human cho  
 Aab56362 Non-endog  
 Abb99724 Amino aci  
 Abb99724 Novel hum  
 Aab30141 Novel hum  
 Aab30141 Novel hum  
 Aab50214 Human tra  
 Aau77171 Human tra  
 Abp23449 Novel hum  
 Abg97480 Human NOV  
 Abp64894 Drosophil  
 Aag70914 S cerevis  
 Abp3936 Candida a  
 Abd13922 Xylinase  
 Adl06072 M. catarr  
 Aau7420 Novel sig  
 Adp94128 Human nov  
 Aaa30801 Novel hum  
 Abg121207 Novel hum  
 Abp57864 Drosophil  
 Abp5947 Drosophil  
 Aay52383 Pseudomon  
 Abp72728 Pseudomon  
 Adp25450 Plasmid  
 Adp25450 Plasmid  
 Aam33522 Human imm  
 Aam33522 Human imm  
 Adh6983 Enterococ  
 Adh47320 Thermococ  
 Adj48530 Oil-absoc  
 Adj48530 Oil-absoc  
 Aab07552 Amino aci  
 Adj33724 Protein o  
 Adj33723 Protein o  
 Adp07447 Novel hum  
 Aap60547 Segment 8

99	41	41.4	326	7	ADB36761	Rheaus	PN	WO2002198920-A1.
100	41	41.4	399	4	ABG19483	Novel hum	XX	
101	41	41.4	487	4	AAM01109	Beta-amyl	PD	12-DEC-2002.
102	41	41.4	494	5	ABBS5478	Lactococc	XX	
103	41	41.4	540	8	ADJ4637	Oil-assoc	PF	31-MAY-2002; 2002WO-US017402.
104	41	41.4	542	8	ADJ4616	Oil-assoc	XX	
105	41	41.4	569	6	ABU3742	Protein e	PR	01-JUN-2001; 2001US-0295449P.
106	41	41.4	602	4	ABG07448	Novel hum	PR	04-JUN-2001; 2001US-0295907P.
107	41	41.4	624	5	ABP73354	Candida a	XX	
108	41	41.4	721	7	ADJ70091	Human hea	PA	(BIOT ) BIOPEN INC.
109	41	41.4	790	4	ABU5243	Human sig	PA	(GEHO ) GEN HOSPITAL CORP.
110	41	41.4	790	5	AAB23390	Human int	XX	
111	41	41.4	790	7	ADB73262	Prostate	PT	
112	41	41.4	871	3	AAB41558	Human ORF	XX	
113	41	41.4	871	4	AAM08936	Human pol	DR	
114	41	41.4	925	2	ABR21606	Aar38936 Human pol	XX	
115	41	41.4	947	6	ABU11694	Human MDD	XX	
116	41	41.4	947	6	ABU11527	Human MDD	XX	
117	41	41.4	956	3	ARY9752	New malto	PT	
118	41	41.4	1281	5	ABG32157	N-methyl	PT	
119	41	41.4	1350	4	AAU02944	Angiotensin	XX	
120	41	41.4	1455	2	ABR23824	Murine ma	PS	
121	41	41.4	1464	2	ABR66039	Aar60339 Human N-m	XX	
122	41	41.4	1464	2	ABR5529	Aar5529 Human NMD	CC	
123	41	41.4	1464	2	ABR80970	Aax80970 Human exc	CC	
124	41	41.4	1464	2	ABW83576	Aaw83576 Human N-m	CC	
125	41	41.4	1464	3	AAY56113	Aay56113 Human NMD	CC	
126	41	41.4	1464	3	ABR26215	Aab26215 Human N-m	CC	
127	41	41.4	1464	5	ABR58507	Abs6507 Human NMD	CC	
128	41	41.4	1464	5	AAO18063	Aao18063 Human NMD	CC	
129	41	41.4	1464	5	ABG33158	Abg33158 N-methyl	CC	
130	41	41.4	1464	6	ABU65878	Abu65878 Human N-m	XX	
131	41	41.4	1464	6	ABU61423	Abu61423 Human N-m	XX	
132	41	41.4	1464	6	ABU03575	Abu03575 Human exp	XX	
133	41	41.4	1464	6	ABU03574	Abu03574 Human exp	XX	
134	41	41.4	1464	6	ABU03577	Abu03577 Human exp	XX	
135	41	41.4	1464	6	ABU03572	Abu03572 Human exp	XX	
136	41	41.4	1464	6	ABU03579	Abu03579 Human exp	XX	
137	41	41.4	1464	6	ABU03571	Abu03571 Human exp	XX	
138	41	41.4	1464	6	ABU03576	Abu03576 Human exp	XX	
139	41	41.4	1464	6	ABU03580	Abu03580 Human exp	XX	
140	41	41.4	1464	6	ABU03570	Abu03570 Human exp	XX	
141	41	41.4	1464	6	ABU51660	Abu51660 Human N-m	RESULT 2	
142	41	41.4	1464	6	ABU4070	Abu4070 Human NMD	ID	AAQ26673
143	41	41.4	1464	7	AEE39234	Human NMD	ID	AAQ26673
144	41	41.4	1464	7	ABB64827	Drosophili	XX	
145	41	41.4	1970	4	ADL05841	M. catarr	AC	AAQ26673;
146	40	40.4	126	8	ADL05841	Aago1614 Human sec	XX	
147	40	40.4	141	3	ANG01614	Abg5062 Novel hum	XX	
148	40	40.4	149	4	ARG05062	Aar3595 Almond N-	DE	20-MAR-2003 (first entry)
149	40	40.4	161	2	ARR93595	Aar93595 Almond N-	DE	Monoclonal antibody binding epitope, SEQ ID No 1.
150	40	40.4	161	2	AAR93595	Homo sapiens.	XX	Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer; binding epitope.
<b>RESULT 1</b>								
ID	AAO26687	AAO26687 standard; Peptide; 18 AA.	XX	PN	WO2002198920-A1.			
AC	AAO26687;		XX	PD	12-DEC-2002.			
DT	20-MAR-2003 (first entry)		XX	PF	31-MAY-2002; 2002WO-US017402.			
XX	Human KIM-1 mucin domain related peptide, SEQ ID No 15.		XX	PR	01-JUN-2001; 2001US-0295449P.			
XX	Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.		XX	PR	04-JUN-2001; 2001US-0295907P.			
XX	Synthetic.		XX	PA	(BIOT ) BIOPEN INC.			
OS			XX	PA	(GEHO ) GEN HOSPITAL CORP.			
			XX	PI	Bailly V, Bonventre J;			

## ALIGNMENTS

DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Claim 4; Page 25; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a binding epitope of the invention  
 XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 99; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QV 1 SSDGLWNNNQNOTQFLEHS 18  
 Db 1 SSDGLWNNNQNOTQFLEHS 18

RESULT 3 Amino acid sequence 81 AA.

CC polypeptide. This sequence represents a human KIM-1 mucin domain protein  
 CC of the invention  
 XX Sequence "81 AA;"  
 SQ Query Match 100.0%; Score 99; DB 6; Length 81;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QV 1 SSDGLWNNNQNOTQFLEHS 18  
 Db 1 SSDGLWNNNQNOTQFLEHS 72

RESULT 4 Amino acid sequence 263 AA.

AC ADE36629;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX Human NOVIC protein SEQ ID NO:39.  
 DE Human NOVIC protein SEQ ID NO:39.  
 KW human; NOX; cytostatic; antiinflammatory; gene therapy; vaccine;  
 KW renal cancer; inflammation; tissue typing.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX  
 PN WO200300856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 19-MAR-2003; 2003WO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 XX  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;  
 PI Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX  
 DR WPI; 2003-876927/81.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or  
 PT preventing a pathology associated with NOX polypeptide e.g. renal cancer  
 PT or inflammation, or for tissue typing.  
 XX  
 PS Example 9; SEQ ID NO 39; 239pp; English.

CC The present invention describes an isolated human NOX polypeptide, where  
 CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at  
 CC least 95 % identical to it, or a sequence comprising one or more  
 CC conservative substitutions in the amino acid sequence. The NOX  
 CC polypeptide, and nucleic acid sequence encoding it, has cytostatic and  
 CC antiinflammatory activities, and can be used in gene therapy, and in  
 CC vaccines. The NOX polypeptide is useful for preparing a composition for  
 CC treating or preventing a pathology associated with NOX polypeptide e.g.  
 CC renal cancer or inflammation, or for tissue typing. The present sequence  
 CC represents a protein sequence which is used in an example from the  
 CC present invention.

XX Sequence 263 AA;

Query Match 100.0%; Score 99; DB 7; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QV 1 SSDGLWNNNQNOTQFLEHS 18  
 Db 1 SSDGLWNNNQNOTQFLEHS 261

**RESULT 5**  
 AD3622  
 ID ADE3622 standard; protein; 263 AA.  
 XX  
 AC ADE36622;  
 XX  
 DT 29-JAN-2004 (first entry)  
 PD 02-OCT-2003.  
 XX  
 DE Plasmid pCR2.1-CG57008-02-S84a 13A protein insert SEQ ID NO:32.  
 XX  
 KW human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;  
 renal cancer; inflammation; tissue typing.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003080856-A2.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 PR 19-MAR-2002; 2002US-0365491P.  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Lepley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Meari M;  
 PI Ooi CB, Anderson DW, Guo X, Giot L, Starling G;  
 XX  
 DR WPI; 2003-876927/81.  
 DR N-PSDB; ADE36621.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or  
 preventing a pathology associated with NOVX polypeptide e.g. renal cancer  
 or inflammation, or for tissue typing.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or  
 preventing a pathology associated with NOVX polypeptide e.g. renal cancer  
 or inflammation, or for tissue typing.  
 XX  
 PS Example 2; SEQ ID NO 32; 239pp; English.  
 XX  
 CC The present invention describes an isolated human NOVX polypeptide, where  
 CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at  
 least 95 % identical to it, or a sequence comprising one or more  
 conservative substitutions in the amino acid sequence. The NOVX  
 polypeptide, and nucleic acid sequence encoding it, has cytostatic and  
 antiinflammatory activities, and can be used in gene therapy, and in  
 vaccines. The NOVX polypeptide is useful for preparing a composition for  
 treating or preventing a pathology associated with NOVX polypeptide e.g.  
 CC renal cancer or inflammation, or for tissue typing. The present sequence  
 CC represents human NOVIC from the present invention.  
 XX  
 SQ Sequence 263 AA;

Query Match	100.0%	Score	99	DB	7	Length	263
Best Local Similarity	100.0%	Pred. No.	8.2e-07	Mismatches	0	Indels	0
Matches	18	Conservative	0	Mismatches	0	Indels	0
Gaps	0						

OY 1 SSDGLWNNTQOLFLEHS 18  
 Db 244 SSDGLWNNTQOLFLEHS 261

**RESULT 6**  
 AD36596  
 ID ADE36596 standard; protein; 263 AA.  
 AC ADE36595;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOVX protein SEQ ID NO:6.  
 XX

**RESULT 7**  
 AAWJ8336  
 ID AAM38336 standard; protein; 334 AA.  
 AC AAWJ8336;  
 XX  
 DT 21-MAY-1998 (first entry)  
 XX  
 DE Human kidney injury related molecule (KIM).  
 XX  
 KW Kidney injury related molecule; KIM; human; renal disease; injury;  
 KW nephritis; tissue regeneration; therapy; monoclonal antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO744460-A1.  
 XX  
 PR 27-NOV-1997.  
 XX  
 PR 23-MAY-1997; 97WO-US009303.  
 XX  
 PR 24-MAY-1996; 96US-0018228P.  
 PR 23-AUG-1996; 96US-0023442P.

PR 04-JUN-2001; 2001US-0295907P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PT (BIOJ ) BIOGEN INC.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Bailey V; Bonventre J;  
 XX  
 DR WPI; 1998-018514/02.  
 XX  
 PT DNA encoding kidney injury related molecule - which is upregulated in injured or regenerating tissue, useful to promote growth of new tissue and survival of damaged tissue.  
 XX  
 PS Claim 9; Page 46-47; 69pp; English.  
 XX  
 CC This protein, designated kidney injury related molecule (KIM), is up-regulated in injured or regenerating tissue. Its amino acid sequence was deduced from a clone (see ATG6035) obtained from a human embryonic liver library. A 572-amino acid (see AW3834) and a 307-amino acid rat KIM (see AW3834) are also claimed. Recombinant KIM polypeptides can be expressed in prokaryotic and eukaryotic host cells using a claimed process. Soluble variants fused to a toxin, imageable compound or radionuclide, and IgG fusion proteins are also claimed. KIM, or an agonist, can be used to treat renal disease and to promote the growth of new tissue or the survival of damaged tissue, generally in conditions where the binding of specific ligand to KIM stimulates cell growth, maintains cellular differentiation or reduces apoptosis, e.g. in cases of renal failure, nephritis, kidney transplants, toxic or hypoxic injury. A monoclonal antibody specific for KIM can be used to treat renal disease, e.g. where binding of KIM to ligand results in neoplasia, loss of cellular function, susceptibility to apoptosis or promotion of inflammation, deliver imaging agents to KIM expressing cells in vivo or in vitro and measure KIM concentration by immunoassay.  
 CC Damage/Regeneration of renal cells can be determined by measuring KIM, particularly to diagnose or monitor the progress of disease or therapy. KIM-expressing tumour cells can be inhibited by treatment with a fusion protein comprising KIM ligand or Mab with a toxin or radionuclide, and tumour cells that express KIM ligand can be inhibited with similarly tagged KIM or anti-KIM ligand antibody  
 XX  
 SQ Sequence 334 AA;

Query Match	100.0%	Score	99	DB	2	Length	334
Best Local Similarity	100.0%	Pred. No.	1.1e-06				
Matches	18	Prod. No.					
Conservative	0	Mismatches	0				
Indels	0	Gaps	0				
Db	264	SSDGIAWNNTQTLFLEHS	281				

RESULT 9  
 AD836618  
 ID AD836618 standard; protein; 339 AA.  
 XX  
 AC AD836618;  
 AC  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Plasmid PCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.  
 XX  
 KW human; NOVX; cytotoxic; antiinflammatory; gene therapy; vaccine; KW  
 KW renal; cancer; inflammation; tissue typing.  
 KW  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 PN WO2003080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PP 19-MAR-2003; 2003HO-US008490.  
 XX  
 PR 19-MAR-2002; 2002US-0365491P.  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PR (CURA-) CURAGEN CORP.  
 XX  
 PR Legley DM, Rieger DK, Tse K, Rastelli L, Smithson G, Mesri M;  
 PR Ooi CE, Anderson DW, Guo X, Giot L, Starling G;  
 XX  
 DR WPI; 2003-876927/81.  
 XX  
 DR N-PSDB; ADB36617.  
 XX  
 PT New polypeptide, useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. renal cancer or inflammation, or for tissue typing.  
 XX  
 PR 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.

RS Example 1; SEQ ID NO 28; 239pp; English.

XX

CC The present invention describes an isolated human NOVX polypeptide, where

CC X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at

CC least 95 % identical to it, or a sequence comprising one or more

CC conservative substitutions in the amino acid sequence. The NOVX

CC polypeptide, and nucleic acid sequence encoding it, has cytosatic and

CC antiinflammatory activities, and can be used in gene therapy, and in

CC vaccines. The NOVX polypeptide is useful for preparing a composition for

CC treating or preventing a pathology associated with NOVX polypeptide e.g.

CC renal cancer or inflammation, or for tissue typing. The present sequence

CC represents a pCR2.1-CG51008-03-SB43 15B protein insert, which is used in

CC an example from the present invention.

XX SQ Sequence 339 AA;

Query Match 100.0%; Score 99; DB 7; Length 339;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDGLWNNTQLEHs 18

Db 244 SSDGLWNNTQLEHs 261

RESULT 10

ADB36592

ID ADB36592 standard; protein; 339 AA.

XX

AC ADB36592;

XX

DT 29-JAN-2004 (First entry)

XX Human NOVIA Protein SEQ ID NO:2.

XX

KW human; NOVX; cytostatic; antiinflammatory; gene therapy; vaccine;

KW renal cancer; inflammation; tissue typing.

XX OS Homo sapiens.

XX DE Human cancer related protein SEQ ID NO:239.

XX DT 09-JUL-2003 (first entry)

XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

KW heart disease; atherosclerosis; endometriosis.

XX OS Homo sapiens.

XX PN WO2003025138-A2.

XX PD 27-MAR-2003.

XX

PR 17-SEP-2002; 2002WO-US029560.

XX PR 17-SEP-2001; 2001US-0323463P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350663P.

PR 08-FEB-2002; 2002US-0355143P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Gish KC, Hevezsi PA, Mack DH, Wilson KE;

XX PI Zlotnick A;

XX DR WPI; 2003-354600/33.

XX DR N-PSDB; ACCT2709.

XX

PT New genes that are up-regulated or down-regulated in cancers, useful as

PT markers for diagnosing e.g. cancer, ischæmia or heart diseases, or as

PT therapeutic targets for screening drugs for treating these diseases.

XX

PS Claim 12; Page 742; 767pp; English.

XX

CC The present invention describes an isolated nucleic acid molecule, which

CC comprises the sequence of any of the genes that are up-regulated or down-

CC regulated in specific cancers (e.g. about 1031 genes up-regulated in

CC acute lymphocytic Leukemia). ACC72641 to ACC72660 represent cancer

CC related gene nucleotide sequences which encode the proteins given in

CC ABR58521 to ABR58709. Also described: (1) determining the presence or

CC absence of a pathological cell in a patient; (2) an expression vector

CC comprising a nucleic acid molecule described above; (3) a host vector

CC comprising the vector; (4) an isolated polypeptide, which is encoded by

CC the nucleic acid; (5) an antibody that specifically binds the polypeptide

CC of (4); (6) specifically targeting a compound to a pathological cell in a

CC patient by administering to the patient the antibody above; and (7) a

CC drug screening assay. The nucleic acid is useful as diagnostic markers or

CC therapeutic targets. In particular, the nucleic acid is useful for

CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,

CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,

CC pancreas, prostate, skin and uterus), wounds, ischæmia, heart diseases,

CC atherosclerosis and endometriosis. The nucleic acid is also useful in

CC drug screening, particularly for identifying agents for treating these

CC represents human NOVIA from the present invention.

CC pathologies  
 XX SQ Sequence 359 AA;

Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 CC 1 SSDGLWNNTQFLLEHS 18  
 CC 264 SSDGLWNNTQFLLEHS 281  
 XX SQ Sequence 359 AA;

RESULT 12  
 ABP70439  
 ID ABP70439 standard; protein; 359 AA.  
 XX AC ABP70439;  
 XX DT 22-APR-2003 (first entry)  
 XX DE Amino acid sequence of human TIM-1 allele 1.  
 XX KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;  
 KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;  
 KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;  
 KW allergic T cell response; autoimmune disease.  
 XX OS Homo sapiens.  
 XX PN WO200302722-A2.  
 XX PD 09-JAN-2003.  
 XX PP 01-JUL-2002; 2002WO-US020890.  
 XX PR 29-JUN-2001; 2001US-030234P.  
 XX PA (STRD ) UNIV LEELAND STANFORD JUNIOR.  
 XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 DR N-PSDB; ABZ68333.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and  
 PT Mucin domain gene sequences, useful for treating cancer or asthma,  
 PT allergy, eczema or autoimmune disease.  
 XX PS Claim 10: Page 80-81; 94pp; English.  
 XX The present sequence is a human T cell immunoglobulin domain and mucin  
 CC domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2,  
 CC TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with  
 CC conserved IgV and mucin domains. The locus comprising the TIM family is  
 CC genetically associated with immune dysfunction, including asthma. The TIM  
 CC gene family is located within a region of human chromosome 5 that is  
 CC commonly deleted in malignancies and myelodysplastic syndrome. Variants  
 CC of TIM-1 and TIM-3 are associated with susceptibility to airway  
 CC hyperreactivity and allergic T cell responses, and other variants  
 CC associated with protection against these responses. T cells express TIM  
 CC proteins, which critically regulate CD4 T cell differentiation. Th1 cells  
 CC preferentially express TIM-3, while Th2 cells preferentially express TIM-  
 CC 1. TIM polypeptides and polynucleotides are useful for treating cancer,  
 CC asthma, allergies, eczema or autoimmune diseases  
 XX SQ Sequence 359 AA;

Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
 CC 1 SSDGLWNNTQFLLEHS 18  
 CC 264 SSDGLWNNTQFLLEHS 281  
 XX SQ Sequence 359 AA;

RESULT 14  
 ABR48174  
 ID ABR48174 standard; protein; 359 AA.  
 XX AC ABR48174;

XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human bladder cancer associated protein sequence SEQ ID NO:64.  
 XX  
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003003906-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PR 03-JUL-2002; 2002WO-US021338.  
 XX  
 PR 03-JUL-2001; 2001US-0302814P.  
 XX  
 PR 03-AUG-2001; 2001US-0310099P.  
 XX  
 PR 08-NOV-2001; 2001US-0341705P.  
 PR 13-NOV-2001; 2001US-0306666P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PT (CURA-) CURAGEN CORP.  
 PI Mack DH, Aziz N;  
 XX  
 DR WPI; 2003-201532/19.  
 DR N-PADB; ACC50985.  
 XX  
 PT Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.  
 XX  
 PS Claim 10; Page 252; 307pp; English.  
 CC The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of Sequences (see ACC5051 to ACC5109). ACC5051 to ACC5109 encode the human bladder cancer-associated proteins given in ABR48146 to AB48242. Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications  
 CC Sequence 359 AA;  
 XX  
 SQ Query Match 100.0%; Score 99; DB 6; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 SSDGLWNNTQTLFLEHS 18  
 Db 264 SSDGLWNNTQTLFLEHS 281  
 RESULT 16  
 ADB36594 standard; protein; 359 AA.  
 XX  
 AC ADB36594;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE Human NOV1b protein SEQ ID NO:4.  
 XX  
 DE Human NOV1b protein SEQ ID NO:4.  
 KW human; NOV1; cytostatic; antiinflammatory; gene therapy; vaccine;  
 KW renal; cancer; inflammation; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20030080856-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PR 19-MAR-2003; 2003WO-US008490.  
 PR 19-MAR-2002; 2002US-0365491P.  
 PR 13-SEP-2002; 2002US-0410618P.  
 XX  
 PA (CURA-) CURAGEN CORP.

PI Lepley DM, Rieger DK, Tse K, Restelli L, Smithson G, Meiri M; PR 05-JUN-2002; 2002US-0386614P.  
 PI Ooi CE, Anderson DW, Guo X, Giot L, Starling G; PR 16-JUL-2002; 2002US-0386839P.  
 XX WPI: 2003-87627/81. PR 22-JUL-2002; 2002US-039775P.  
 DR N-PSDB; ADB36593. PR 22-JUL-2002; 2002US-039785P.  
 XX PT New polypeptide, useful for preparing a composition for treating or PR 09-SEP-2002; 2002US-0409450P.  
 PT preventing a pathology associated with NOVX polypeptide e.g. renal cancer PR (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX or inflammation, or for tissue typing. PR AFar D, Aziz N, Ginsburg WM, Gish KC, Glynnne R, Hevezzi PA;  
 XX PS Claim 1; SEQ ID NO 4; 239pp; English. PR Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 XX CC The present invention describes an isolated human NOVX polypeptide, where PR DR WPI: 2003-46849/44.  
 XX X is 1a to 1d or 2a to 2h, or its mature form, a sequence that is at PR N-PSDB; ADN38983.  
 CC least 95 % identical to it, or a sequence comprising one or more PR PT conservative substitutions in the amino acid sequence. The NOVX PR PT polypeptide, and nucleic acid sequence encoding it, has cytostatic and  
 CC antiinflammatory activities, and can be used in gene therapy, and in PR XX vaccines. The NOVX polypeptide is useful for preparing a composition for PR PS treating or preventing a pathology associated with NOVX polypeptide e.g.  
 CC renal cancer or inflammation, or for tissue typing. The present sequence PR XX represents human Novib from the present invention.  
 XX SQ Sequence 359 AA:  
 Query Match 100.0%; Score 99; DB 7; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SSDGLWNNTQOLFLEHS 18  
 Db 264 SSDGLWNNTQOLFLEHS 281  
 RESULT 17  
 ID ADN38984  
 ID ADN38984 standard; protein; 359 AA.  
 AC ADN38984;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.  
 XX KW Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
 KW vulvarian; gene therapy; vaccine.  
 OS Homo sapiens.  
 XX PN WO2003042661-A2.  
 XX DT 22-MAY-2003.  
 XX PD 13-NOV-2002; 2002WO-US036810.  
 PR 13-NOV-2001; 2001US-035066P.  
 PR 11-NOV-2001; 2001US-0322464P.  
 PR 29-NOV-2001; 2001US-0334393P.  
 PR 01-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0310376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0336714P.  
 PR 20-FEB-2002; 2002US-0355077P.  
 PR 29-MAR-2002; 2002US-0368809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0386839P.  
 PR 22-JUL-2002; 2002US-039775P.  
 PR 22-JUL-2002; 2002US-039785P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 PR (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX XX WPI: 2003-46849/44.  
 PR PR AFar D, Aziz N, Ginsburg WM, Gish KC, Glynnne R, Hevezzi PA;  
 PR PR Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 PR XX DR WPI: 2003-46849/44.  
 PR N-PSDB; ADN38983.  
 PR PT Determining the presence or absence of a pathological cell in a patient,  
 PR whose expression is upregulated or downregulated in specific cancers or  
 PR other diseases such as angiogenic or fibrotic disorders, and to methods  
 PR of determining the presence or absence of a pathological cell in a  
 PR patient by detecting a nucleic acid at least 80% identical to those of  
 PR the invention or by detecting a polypeptide of the invention. The  
 PR invention also relates to expression vectors and host cells comprising a  
 PR nucleic acid of the invention; antibodies which specifically bind a  
 PR polypeptide of the invention; use of such antibodies for drug targeting;  
 PR methods of screening for modulators of activity or expression of the  
 PR polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 PR antibodies and methods are useful for diagnosing, prognosis and treating  
 PR cancer and other conditions such as psoriasis, ischaemia, heart disease,  
 PR atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 PR neovascularisation syndromes, scarring and uterine fibroids. They may  
 PR also be useful in wound healing and in contraction. The present  
 PR sequence represents a polypeptide of the invention. The present  
 PR sequence 359 AA;  
 PR XX SQ Sequence 359 AA:  
 PR Query Match 100.0%; Score 99; DB 7; Length 359;  
 PR Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 PR Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PR QY 1 SSDGLWNNTQOLFLEHS 18  
 PR Db 264 SSDGLWNNTQOLFLEHS 281  
 RESULT 18  
 ID ABP70443  
 ID ABP70443 standard; protein; 364 AA.  
 XX AC ABP70443;  
 XX AC ABP70443;  
 XX DT 22-APR-2003 (first entry)  
 XX DE Amino acid sequence of human TIM-1 allele 6.  
 XX PR T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3;  
 KW TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema;  
 KW myelodysplastic syndrome; airway hyperreactivity; cancer; asthma;  
 KW allergic T cell response; autoimmune disease.  
 OS Homo sapiens.  
 XX PR Key Location/Qualifiers  
 FT Misc-difference 123 /note= "encoded by GAG"  
 FT Misc-difference 161 /note= "encoded by GACT"  
 FT Misc-difference 201 /note= "encoded by ACAGT"

XX WO2003002722-A2.  
 XX 09-JAN-2003.  
 XX PR 01-JUL-2002; 2002WO-US020890.  
 XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX PT McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 XX DR N-PSDB; ABZ69336.  
 XX PR WPI; 2003-210268/20.  
 XX DR N-PSDB; ABZ69336.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma, allergy, eczema or autoimmune disease.  
 XX PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma, allergy, eczema or autoimmune disease.  
 XX PS Claim 10, Page 87-88; 94pp; English.  
 XX CC The present sequence is a human T cell immunoglobulin domain and mucin domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2, TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with conserved IgV and mucin domains. The locus comprising the TIM family is genetically associated with immune dysfunction, including asthma. The TIM gene family is located within a region of human chromosome 5 that is commonly deleted in malignancies and myelodysplastic syndrome. Variants of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and allergic T cell responses, and other variants associated with protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. Th1 cells preferentially express TIM-3, while Th2 cells preferentially express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases.  
 XX CC Of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and allergic T cell responses, and other variants associated with protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. Th1 cells preferentially express TIM-3, while Th2 cells preferentially express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases.  
 XX SQ Sequence 364 AA;  
 Query Match 100.0%; Score 99; DB 6; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; N mismatches 0; N indels 0; N gaps 0;  
 Qy 1 SDGGLWNNTQFLLEHS 18  
 Db 269 SSDGLWNNTQFLLEHS 286  
 RESULT 19  
 ABP70442 ID ABP70440 standard; protein; 365 AA.  
 XX AC ABP70440;  
 XX DT 22-APR-2003 (first entry)  
 DE Amino acid sequence of human TIM-1 allele 3.  
 XX T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3; TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema; myelodysplastic syndrome; airway hyperreactivity; cancer; asthma; allergic T cell response; autoimmune disease.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 208 /note= "encoded by RCG"  
 XX PN WO2003002722-A2.  
 XX PD 09-JAN-2003.  
 XX PR 01-JUL-2002; 2002WO-US020890.  
 XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
 XX DR WPI; 2003-210268/20.

DR N-PSDB; ABZ68334.

XX

PT New nucleic acid comprising a mammalian T cell immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma,

PT allergy, eczema or autoimmune disease.

PS Claim 10; Page 83-84; 94pp; English.

The present sequence is a human T cell immunoglobulin domain and mucin domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2, TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with conserved IgV and mucin domains. The locus comprising the TIM family is genetically associated with immune dysfunction, including asthma. The TIM gene family is located within a region of human chromosome 5 that is commonly deleted in malignancies and myelodysplastic syndrome. Variant B of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and allergic T cell responses, and other variants associated with protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. Th1 cells preferentially express TIM-3, while Th2 cells preferentially express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases

SQ Sequence 365 AA;

Query Match 100.0%; Score 99; DB 6; Length 365;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06; Mismatches 0; Indels 0; Gaps 0;

Qv 1 SSDGLWNNTNOTQLEHS 18  
Db 270 SSDGLWNNTNOTQLEHS 287

RESULT 21

ID ABP70441  
AC ABP70441;  
XX

DT 22-APR-2003 (first entry)  
XX

DE Amino acid sequence of human TIM-1 allele 4.  
XX

KW T cell immunoglobulin domain; mucin domain; TIM; TIM-1; TIM-2; TIM-3; TIM-4; immune dysfunction; chromosome 5; malignancy; allergy; eczema; myelodysplastic syndrome; airway hyperreactivity; cancer; asthma; allergic T cell response; autoimmune disease.

XX OS Homo sapiens.

PH Key Location/Qualifiers  
PT Misc-difference 172

PT Misc-difference 202 /note= "encoded by GACT"

PT Misc-difference 240 /note= "encoded by T"

PT Misc-difference 270 /note= "encoded by GCA"

PT Misc-difference 270 /note= "encoded by ART"

XX WO2003002722-A2.

XX PD 09-JAN-2003.

XX PF 01-JUL-2002; 2002WO-US020890.  
XX PR 29-JUN-2001; 2001US-0302344P.

XX PA (SIRD ) UNIV LELAND STANFORD JUNIOR.

XX PI McIntire JJ, Dekruyff RH, Umetsu DT, Freeman GJ, Kuchroo V;  
XX

DR WPI; 2003-210268/20.

N-PSDB; ABZ68335.

PT New nucleic acid comprising a mammalian T cell Immunoglobulin domain and mucin domain gene sequences, useful for treating cancer or asthma,

PT allergy, eczema or autoimmune disease.

PS Claim 10; Page 84-85; 94pp; English.

The present sequence is a human T cell immunoglobulin domain and mucin domain-1 (TIM-1) polypeptide. The specification describes TIM-1, TIM-2, TIM-3 and TIM-4. TIM polypeptides are cell surface molecules with conserved IgV and mucin domains. The locus comprising the TIM family is genetically associated with immune dysfunction, including asthma. The TIM gene family is located within a region of human chromosome 5 that is commonly deleted in malignancies and myelodysplastic syndrome. Variants of TIM-1 and TIM-3 are associated with susceptibility to airway hyperreactivity and allergic T cell responses, and other variants associated with protection against these responses. T cells express TIM proteins, which critically regulate CD4 T cell differentiation. Th1 cells preferentially express TIM-3, while Th2 cells preferentially express TIM-1. TIM polypeptides and polynucleotides are useful for treating cancer, asthma, allergies, eczema or autoimmune diseases

SQ Sequence 359 AA;

Query Match 94.9%; Score 94; DB 6; Length 359;  
Best Local Similarity 94.4%; Pred. No. 6.6e-06; Mismatches 1; Indels 0; Gaps 0;

Qv 1 SSDGLWNNTNOTQLEHS 18  
Db 264 SSDGLWNNTNOTQLEHS 281

RESULT 22

ID AAR92803  
ID AAR92803 standard; protein; 451 AA.  
XX

AC AAR92803;

DT 24-MAY-1996 (first entry)  
XX

DE Hepatitis A virus receptor.  
XX

KW Hepatitis A virus; receptor; HAV; diagnosis; therapy; vaccine;

KW transgenic animal.

XX OS Cercopithecus aethiops.

XX PN WO904376-A1.

XX PD 15-FEB-1996.

XX PF 04-AUG-1995; 95WO-US009941.

XX PR 05-AUG-1994; 9409-00287001.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kaplan G, Feinstein SM;

XX WPI; 1996-129392/13.

XX DR N-PSDB; AAT17864.

PT DNA encoding Hepatitis A virus receptor and its fragments - useful for the detection, diagnosis, prevention and treatment of HAV infection.  
XX  
PS Claim 1; Page 39-41; 52pp; English.

XX A hepatitis A virus (HAV) receptor (AAR92803) was identified as the product of a nucleic acid sequence isolated from HAV-infected primary African green monkey kidney cells. Recombinant receptor can be produced

CC in large amounts by expression of the nucleic acid in prokaryotic or eukaryotic host cells or in transgenic animals. It can be used in the detection, prevention and treatment of HAV infection, in methods of purifying or removing HAV from samples, and methods of determining the anti-HAV activity of caps. Expression in transgenic animals provides a method for testing vaccine efficacy

XX SQ Sequence 451 AA;

Qy 1 SDGGLWNNNOTQLELHS 18  
Db 344 SSDGLWNNNOTQLSPEHS 361

RESULT 23

AQ026686  
ID AAO26686 standard; peptide; 18 AA.

XX AC AAC26686;  
XX DT 20-MAR-2003 (first entry)

XX Human KIM-1 mucin domain related peptide, SEQ ID No 14.

XX KW Cyrostatic; gene therapy; antibody; antigen; antigen-binding; proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.

XX OS Synthetic.

PN WO200299920-A1.

XX PD DR 12-DEC-2002.

XX PR 01-JUN-2001; 2001US-0205907P.

XX PR 04-JUN-2001; 2001US-0205907P.

XX PA (BIOJ ) BIOPHARM INC.  
PA (GENO ) GEN HOSPITAL CORP.

XX PT Bailly V, Bonventre J;

XX PS WPI, 2003-156845/15.

XX PT New antibody, antibody derivative or antigen-binding polypeptide that inhibits proteolytic release of a soluble kidney injury molecule-1 polypeptide, useful for treating or preventing renal disease or injury, e.g. renal cancer.

XX DR 31-MAY-2002; 2002WO-US017402.

XX PR 01-JUL-2000; 2000US-0216995P.

XX PR 07-JUL-2000; 2000US-0216995P.

XX PA (ALPH-) ALPHAVAX INC.  
PA (UVMC-) UNIV NORTH CAROLINA.

XX PI Olmsted R, Keith P, Dryga S, Caley I, Maughan M, Johnston R;  
PI Davis N, Swanstrom R;

XX DR WPI; 2002-171664/22.  
DR N-PSDB; AAD25138.

XX PS Example 4; Page 180-183; 201PP; English.

XX The invention relates to a composition comprising isolated nucleic acids encoding env, gag or pol gene product of human immunodeficiency virus or immunogenic fragment of the gene products. The gag gene product is modified to inhibit formation of virus-like particles containing gag gene product and their release from cells, and the pol gene product is modified to inhibit reverse transcriptase activity. The invention also relates to a method for producing an alpha-virus replicon particle used in vaccines. The composition is useful for inducing an immune response to human immunodeficiency virus (HIV) or for treating or preventing HIV infection in a subject. The alpha-virus replicon particle is useful in a vaccine. The composition is useful for administering a protein or peptide to a subject. A composition comprising heparin affinity-purified alpha-virus replicon particle is useful as a clinical trial material and as a commercial product. The present sequence is Venezuelan equine encephalitis virus (VEE) glycoprotein V3014 used in the exemplification of the invention.

XX SQ Sequence 981 AA;

Qy 1 SDGGLWNNNOTQLELHS 16  
Db 489 SLIDLWNNNQOMFWIQ 504

RESULT 25

Query Match 53.5%; Score 53; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDGGLWNN 9

ID AAO26688 standard; peptide; 18 AA.  
 XX  
 AC AAO26688;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX Human KIM-1 mucin domain related peptide, SEQ ID No 16.  
 KW Cytostatic; gene therapy; antibody; antigen; antigen-binding;  
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
 KW renal disease; injury; renal cancer.  
 OS Synthetic.  
 PA (JANCO ) JANSSEN PHARM NV.  
 XX WO20029920-A1.  
 PN XX  
 XX 12-DEC-2002.  
 PD XX  
 PP 31-MAY-2002; 2002WO-US017402.  
 XX PR 01-JUN-2001; 2001US-0295449P.  
 PR 04-JUN-2001; 2001US-0295907P.  
 XX PA (GENO ) GEN HOSPITAL CORP.  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX PT Bailey V, Bonventre J;  
 XX DR WPI; 2003-156845/15.  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT initiates proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX PS Disclosure; Fig 1A; 42pp; English.  
 XX CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related  
 CC peptide of the invention  
 XX SQ Sequence 18 AA:  
 Query Match 45.5%; Score 46; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 QTQFLEHS 18  
 Db 1 QTQFLEHS 9  
 RESULT 26  
 ABG93049 ABG93049 standard; protein; 508 AA.  
 XX  
 AC ABG93049;  
 XX DT 21-NOV-2002 (first entry)  
 XX DE S. cerevisiae BAX-associated protein fragment SEQ ID 56.  
 XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;  
 KW vasoconstrictor; vaccine; gene therapy; proliferative disorder; cancer;  
 KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;  
 KW neurodegeneration; cell death.  
 XX OS Saccharomyces cerevisiae.

---

XN WO200264766-A2.  
 FN XX  
 FD 22-AUG-2002.  
 XX  
 PR 21-DEC-2001; 2001WO-EP015398.  
 XX PR 22-DEC-2000; 2000EP-00870318.  
 PR 04-JAN-2001; 2001EP-00870002.  
 PR 09-JAN-2001; 2001EP-00870003.  
 XX PA (JANCO ) JANSSEN PHARM NV.  
 XX PI Contreras RH, Eberhardt I, Luyten WHM, Reekmans RJ;  
 XX DR WPI; 2003-667002/71.  
 DR N-PSDB; ABQ76315.  
 XX PR New isolated nucleic acid representing a synthetic Bax-gene, useful as  
 PR medicament for treating, preventing and/or alleviating yeast or fungal  
 PR infections or proliferative disorders, or for preventing apoptosis in  
 PR certain diseases.  
 XX PS Claim 36; Fig 1; 34app; English.  
 XX CC This invention describes a novel nucleic acid representing a synthetic  
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-  
 CC resistant yeast or fungi, identifying, or obtaining and identifying  
 CC Candida spp. sequences that are differentially expressed in a pathway  
 CC eventually leading to programmed cell death or identifying inhibitors or  
 CC inhibitor sequences of Bax-induced cell death. The products of the  
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and  
 CC vasotropin activity and can be used in vaccines or for gene therapy. The  
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,  
 CC antisense molecules and antibodies are useful as medicaments or in  
 CC preparing a medicament for treating, preventing and/or alleviating  
 CC diseases associated with yeast or fungi or proliferative disorders, such  
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds  
 CC or polypeptides, or the genetically modified organism are useful for  
 CC preparing a medicament for modifying the endogenous flora of humans and  
 CC other mammals. The vaccine is useful for immunising against yeast or  
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,  
 CC ischaemia, diseases related with viral infections or neurodegenerations.  
 CC This sequence represents a polypeptide associated with the Bax gene  
 CC described in the disclosure of the invention  
 XX SQ Sequence 508 AA:  
 Query Match 45.5%; Score 46; DB 5; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 WNNNOTQFILE 16  
 Db 160 WNNNNSMIFLE 170  
 RESULT 27  
 ABR52836 ABR52836 standard; protein; 508 AA.  
 XX  
 AC ABR52836;  
 XX DT 20-JUN-2003 (first entry)  
 XX DE Protein sequence #SEQ ID 537.  
 XX KW Multiprotein complex; eukaryote; drug target; diagnosis.  
 XX OS Saccharomyces cerevisiae.  
 XX EP125844-A1.  
 PN XX

PD 20-NOV-2002.  
 XX  
 PF 20-DEC-2001; 2001EP-00130253.  
 XX  
 PR 15-MAY-2001; 2001EP-00111774.  
 XX  
 PA (CELL-) CELLZONE AG.  
 XX  
 PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;  
 XX  
 DR WPI; 2003-250078/25.  
 XX  
 PT New isolated protein complexes useful for diagnosing a disease or  
 PT disorder, or as a target for an active agent of a pharmaceutical,  
 PT preferably a drug target in the treatment or prevention of disease or  
 PT disorder.  
 XX  
 PS Disclosure; SEQ ID NO 537; 17pp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel protein complexes comprising a first and a  
 CC second protein, or its derivative, fragment, homologue or variant. The  
 CC proteins are selected from given protein complexes, which are not defined  
 CC in the specification. The variants are encoded by nucleic acids that  
 CC hybridize to the nucleic acids encoding the proteins under low stringency  
 CC conditions. The protein complexes are useful as targets for an active  
 CC agent of a pharmaceutical. These protein complexes are particularly  
 CC useful as drugs targets for the treatment or preventing of a disease or  
 CC disorder. The complexes and methods above are useful in diagnosing or  
 CC screening for the presence of a disease or disorder or a predisposition  
 CC for developing a disease or disorder in a subject. These are also useful  
 CC in screening for a drug for treatment or prevention of a disease or  
 CC disorder. The molecule that modulates the amount, activity or protein  
 CC components of the complex is useful for the manufacture of a medicament  
 CC for the treatment or prevention of a disease or disorder. This sequence data for  
 CC corresponds to a protein of the invention. (Note: the sequence data for  
 CC this patent did not form part of the printed Specification but was  
 CC obtained from the EPO in electronic format).  
 XX  
 SQ Sequence 508 AA;

Query Match 46.5%; Score 46; DB 6; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 WNNNOTQFILE 16  
 Db 160 WNNNASMFILE 170

RESULT 28  
 ADK62270  
 ID ADK62270 standard; protein; 508 AA.  
 AC  
 AC  
 AC  
 AC  
 AC  
 AC  
 OS 06-MAY-2004 (first entry)  
 XX  
 DB Disease treating protein complex-derived protein #261.  
 XX  
 KW protein complex; drug target; diagnosis.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1338608-A2.  
 XX  
 PD 27-AUG-2003.  
 XX  
 PP 20-DEC-2002; 2002EP-00102902.  
 XX  
 PR 20-DEC-2001; 2001EP-00130253.  
 XX  
 PA (CELL-) CELLZONE AG.  
 XX  
 PA Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J, J.;  
 PT Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
 PT Mitchon A, Leutwein C, Rick J;  
 XX

DR WPI; 2003-638460/61.  
 DR N-PSDB; ADK62271.  
 XX  
 PT New proteins and protein complexes from eukaryotes, useful as targets in  
 PT drug screening, or in diagnosing or screening for the presence of a  
 PT disease or disorder, or a predisposition for developing a disease or  
 PT disorder in a subject.  
 XX  
 PS Disclosure; SEQ ID NO 521; 13pp; English.  
 XX  
 CC The invention relates to novel protein complexes comprising a first and a  
 CC second protein, or its derivative, fragment, homologue or variant. The  
 CC proteins are selected from given protein complexes, which are not defined  
 CC in the specification. The variants are encoded by nucleic acids that  
 CC hybridize to the nucleic acids encoding the proteins under low stringency  
 CC conditions. The protein complexes are useful as targets for an active  
 CC agent of a pharmaceutical. These protein complexes are particularly  
 CC useful as drugs targets for the treatment or preventing of a disease or  
 CC disorder. The complexes and methods above are useful in diagnosing or  
 CC screening for the presence of a disease or disorder or a predisposition  
 CC for developing a disease or disorder in a subject. These are also useful  
 CC in screening for a drug for treatment or prevention of a disease or  
 CC disorder. The molecule that modulates the amount, activity or protein  
 CC components of the complex is useful for the manufacture of a medicament  
 CC for the treatment or prevention of a disease or disorder. This sequence data for  
 CC corresponds to a protein of the invention. (Note: the sequence data for  
 CC this patent did not form part of the printed Specification but was  
 CC obtained from the EPO in electronic format).  
 XX  
 SQ Sequence 508 AA;

Query Match 46.5%; Score 46; DB 7; Length 508;  
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6 WNNNOTQFILE 16  
 Db 160 WNNNASMFILE 170

RESULT 29  
 ABG71366  
 ID ABG71366 standard; protein; 545 AA.  
 AC  
 AC  
 AC  
 AC  
 AC  
 AC  
 DT 28-JAN-2003 (first entry)  
 XX  
 DB Potato plastidic targeted beta-amylase (ppt-beta-amylase).  
 KW Potato; starch degrading enzyme; enzyme; starch degradation;  
 KW washing agent; flushing agent; potato plastidic targeted beta-amylase;  
 KW ppt-beta-amylase.  
 XX  
 OS Solanum tuberosum.  
 PN WO200206112-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PP 25-APR-2002; 2002WO-EP004609.  
 XX  
 PR 25-APR-2001; 2001EP-0011005.  
 XX  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PT Scheidig A, Kossmann J, Froehlich A;  
 PT  
 DR WPI; 2003-058726/05.  
 DR N-PSDB; ABS56813.  
 XX  
 PT Novel nucleic acid useful for modifying starch degradation and as  
 hybridization probes to isolate related genes, encodes enzyme involved in

PT starch degradation.  
 XX  
 PS Claim 1; Page 105-107; 107pp; English.  
 CC The invention relates to a nucleic acid molecule encoding a starch degrading enzyme. The nucleic acid is useful for reducing endogenous activity of a biologically active fragment, for modifying starch degradation, as a hybridisation probe to isolate related genes and as a primer for amplification techniques such as polymerase chain reaction. The nucleic acid is also useful as an agent for starch degradation in a washing or flushing agent. This sequence represents a potato plastidic targeted beta-amylase (PPP-beta-amylase) polypeptide  
 XX SQ Sequence 545 AA;

Query Match	Score	DB	Length
Best Local Similarity	46.5%	6	545
Matches	57.1%	Pred. No.	2e+02
		Mismatches	5
		Indels	0
		Gaps	0

OY 3 DGLMANNQTOFLLE 16  
 Db 324 DGTWNSEYGOFFLE 337

RESULT 30  
 ADJ49214  
 ID ADU49214 standard; protein; 545 AA.  
 XX  
 AC ADJ49214;  
 XX DT 06-MAY-2004 (first entry)  
 DE Oil-associated gene related protein #714.  
 XX oil-associated gene; transgenic; enhanced seed oil; vegetable oil.  
 KW Unidentified.  
 OS  
 XX  
 PN US2004025202-A1.  
 XX  
 PD 05-FEB-2004.  
 PF 14-MAR-2003; 2003US-00399566.  
 XX  
 PR 15-MAR-2002; 2002US-0365301P.  
 PR 26-JUN-2002; 2002US-0391786P.  
 PR 26-JUN-2002; 2002US-0392018P.  
 XX  
 PA (LAUR/ ) LAURIE C.C.  
 PA (RAYA/ ) RAVANELLO M.  
 PA (SAYA/ ) SAVAGE T.  
 PA (LEDE/ ) LEDAUX J.R.  
 PA (ROGE/ ) ROGERS J.A.  
 PT Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA,  
 XX DR WPI; 2004-142683/14.  
 XX  
 PT Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.  
 XX  
 PS Example 3; SEQ ID NO 1218; 22pp; English.  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.

XX SQ Sequence 545 AA;

Query Match	Score	DB	Length
Best Local Similarity	45.5%	8	545
Matches	57.1%	Pred. No.	2e+02
		Mismatches	5
		Indels	0
		Gaps	0

OY 3 DGLMANNQTOFLLE 16  
 Db 324 DGTWNSEYGOFFLE 337

RESULT 31  
 ABR57094  
 ID ABR57094 standard; peptide; 114 AA.  
 XX  
 AC ABR57094;  
 XX DT 26-AUG-2003 (first entry)  
 DE MLHR comparison related RAHRSPLC2 amino acid sequence.  
 XX LHR; MLHR; immunoglobulin; Ig; immunoglobulin heavy chain dimer; ligand-combined partner; cell surface adhesion molecule; ligand; KW lymphocyte cell surface glycoprotein.  
 XX Unidentified.  
 OS  
 PN JP2002325589-A.  
 XX PD 12-NOV-2002.  
 XX PR 21-NOV-1990; 2002JP-00026825.  
 XX PR 22-NOV-1989; 890US-00444625.  
 PR 21-NOV-1990; 91JP-00501520.  
 XX (GETH ) GENENTECH INC.  
 DR WPI; 2003-407283/39.  
 XX PT A fused protein consisting of a ligand-combined protein and a stable plasma protein, a polypeptide, a nucleic acid, a replicable expression vector, a composition.  
 XX  
 PS Example 1; Fig 11; 44pp; Japanese.  
 XX  
 CC The present invention describes a polypeptide (I) containing an immunoglobulin (Ig) heavy chain dimer, having no Ig light chain in which the amino acid sequence of a ligand-combined partner is a receptor, a carrier protein, a hormone, a growth factor, an enzyme or a nutritive substance, but is not a subunit polypeptide encoded by a lymphocyte inducing receptor, an Ig gene superfamily constituting element, a protein homologous to it, or a separated gene substitute of the variable region of at least one Ig heavy chain. Its combined partner is fused with the amino acid sequence of an Ig stationary region at its C-end and maintains its combining feature. Also described: (1) a nucleic acid encoding (I), (2) a replicable expression vector containing the nucleic acid of (1); (3) a composition containing cells transformed by the expression vector of (2); and (4) producing (I), comprising culturing the cells of (3) in which the transformed cells are cultured and the polypeptide is recovered from the cell culture. The polypeptide is useful as a cell surface adhesion molecule and a ligand. In an example from the present invention mouse lymphocyte cell surface glycoprotein designated LHR (MLHR) was isolated from a mouse spleen and purified and cloned. The present sequence represents an amino acid sequence given in comparison with an MLHR amino acid sequence, which is used in an example from the present invention  
 XX Sequence 114 AA;

Query Match Score 45; DB 6; Length 114;  
 Best Local Similarity 72.7%; Pred. No. 53;



QY 3 DGLWNNO---TQFLFH 17  
 Db 81 DGTWINDNQLOEMAQLRIKH 99

RESULT 34  
 ID AAM42108 standard; protein; 244 AA.  
 XX  
 AC AAM42108;  
 DT 22-OCT-001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 7039.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US034263.  
 XX  
 PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-0088725.  
 PR 25-APR-2000; 2000US-0052317.  
 PR 20-JUN-2000; 2000US-059842.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-0053450.  
 PR 14-SEP-2000; 2000US-0062191.  
 PR 19-OCT-2000; 2000US-0093036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX  
 PA (HYSE- ) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D, Wang J, Xu C, Yang Y, Zhang J, Zhao QA,  
 PI Zhou P, Wehrman T, Xu AJ, Yang Y,  
 DR N-PDB: AAI61264.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.  
 XX  
 Example 2; SEQ ID NO 7039; 10078PP; English.  
 CC The invention relates to human nucleic acids (AII5779-AAI61369) and the encoded polypeptides (AII3862-AAI42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 244 AA;  
 45.5%; Score 45; DB 4; Length 244;

Query Match

QY	Best Local Similarity	Pred. No.	Indels	Gaps
Db	Matches	Conservative	Mismatches	1;
QY	3 DGLWNNO---TQFLFH 17	3	4	
Db	81 DGTWINDNQLOEMAQLRIKH 99	3	4	1;
<b>RESULT 35</b>				
ID	AY99671	AY99671 standard; protein; 265 AA.		
XX	AY99671;			
DE	03-NOV-2000 (first entry)			
XX	Human GTPase associated protein-22.			
XX	Guanine nucleotide binding protein; GTP-binding protein; G-protein; GTPase; GTPase associated protein; GTPAP; Cell proliferation; autoimmune; inflammatory; immune system disorder; cancer; AIDS; acquired immune deficiency syndrome; asthma; atherosclerosis; arthritis; systemic lupus erythematosus; psoriasis; human.			
OS	Homo sapiens.			
XX	PN WO20031263-A2.			
XX	PD 02-JUN-2000.			
PR	23-NOV-1999; 99WO-US28013.			
XX	PR 23-NOV-1998; 98US-0109592P.			
PR	04-FEB-1999; 98US-0118610P.			
PR	06-APR-1999; 99US-0127990P.			
XX	(INCY-) INCYTE PHARM INC.			
XX	PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;			
PI	Yang J, Azimzai Y;			
XX	DR WPI; 2000-400073/34.			
DR	N-PDB; AAA49192.			
XX	PT Human GTPase associated proteins, polynucleotides, and antibodies, useful for diagnosing, preventing and treating various diseases such as atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS), asthma, and autoimmune diseases.			
PT	Claim 1; Page 108-109; 144PP; English.			
XX	Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is human GTPAP-22 protein. This sequence was derived from a cDNA library of the htrc2 cell line from a human teratocarcinoma. This protein is expressed in nervous, gastrointestinal and cardiovascular tissue. The GTPAP proteins may be used to define agonists and antagonists of GTPAP activity and to generate antibodies to GTPAP. This means the GTPAP proteins may be useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders, inflammatory disorders, immune system disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis			
SQ	Sequence 265 AA;			
Query Match	Best Local Similarity	45.5%; Score	45; DB	3; Length
Matches	9;	Conservative	3;	Mismatches
QY	3 DGLWNNO---TQFLFH 17			
Db	74 DGTWINDNQLOEMAQLRIKH 92			

RESULT 36  
 ADD46355  
 ID ADD46355 standard; protein; 301 AA.  
 XX  
 AC ADD46355;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Rat Protein P08290, SEQ ID NO 12033.  
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX OS Rattus norvegicus.  
 XX PN WO2003016475-A2.  
 XX PD 27-FEB-2003.  
 XX PP 14-AUG-2002; 2002WO-US025765.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX PA (GERHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX DR WPT; 2003-268312/26.  
 DR GENBANK; P08290.  
 PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
 XX PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification), which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 301 AA;

Query Match 45.5%; Score 45; DB 7; Length 301;  
 Best local Similarity 72.7%; Pred. No. 1; 5e-02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SDGLWNWNGTQ 12  
 YY ||||| : |  
 Db 276 SDGLWNNDFCQ 286

RESULT 37  
 ADD63357  
 ID ADE63357 standard; protein; 301 AA.  
 XX AC ADE63357;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Rat Protein P08290, SEQ ID NO 9295.  
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX OS Rattus norvegicus.  
 XX PI WO2003016475-A2.  
 XX PR 14-AUG-2002; 2002WO-US025765.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX PA (GERHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX DR WPT; 2003-268312/26.  
 DR GENBANK; P08290.  
 PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
 XX PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification), which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 301 AA;

		Query Match Best Local Similarity 72.7%;保守性 8; Mismatches 1; Indels 0; Gaps 0;	Score 45; DB 7; Length 301; Pred. No. 1.5e+02; Mismatches 3; Indels 4; Gaps 1;
b	2 SDGLWNNGTQ 12 276 SDGLWNNDNFQO 286		
	:	:	:
RESULT 38	AAB92470		
X	AAB92470 standard; protein; 309 AA.		
C	AAB92470;		
X	26-JUN-2001 (first entry)		
E	Human protein sequence SEQ ID NO:10536.		
X	Human; primer; detection; diagnosis; antisense therapy; gene therapy.		
X	Homo sapiens.		
N	EP1074617-A2.		
X	07-FEB-2001.		
X	28-JUL-2000; 2000EP-00116126.		
R	29-JUL-1999; 99JP-00248036.		
R	27-AUG-1999; 99JP-00300253.		
R	11-JAN-2000; 2000JP-00118776.		
R	02-MAY-2000; 2000JP-00183677.		
R	09-JUN-2000; 2000JP-00241899.		
X	(HELI-) HELIX RES INST.		
X	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
X	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
X	WPI; 2001-318749/34.		
X	Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.		
S	Claim 8; SEQ ID NO 10536; 2537pp + sequence Listing; English.		
C	The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:		
C	(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the nucleotide sequence defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs readily without any specialised methods. AAB03166 to AAB1628 and AAB13633 to AAB18742 represent human cDNA sequences; AAB93446 to AAB95893 represent human amino acid sequences; and AAB13629 to AAB13632 represent oligonucleotides, all of which are used in the exemplification of the present invention		
X	Sequence 309 AA;		
X	:	:	:
RESULT 39	AABB97591		
ID	AABB97591 standard; protein; 309 AA.		
C	AABB97591;		
X	ABB97591;		
X	27-JUN-2002 (first entry)		
E	Novel human protein SEQ ID NO: 859.		
X	Human; antiaemic; vulnery; antiinflammatory; immunomodulator; antinefertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; anticarotid; protein therapy; EST; expressed sequence tag.		
X	Homo sapiens.		
X	XX		
P	WO200222660-A2.		
D	21-MAR-2002.		
X	PP		
R	10-SEP-2001; 2001WO-US026015.		
R	XX		
R	PR		
R	11-SEP-2000; 2000US-00659671.		
X	XX		
P	(HYSB-) HYSEQ INC.		
X	XX		
P	Tang YT, Liu C, Zhou F, Abundi V, Zhang J, Zhao QA, Ren F;		
P	Xue AJ, Yang Y, Wehrman T, Drmanac RT;		
X	XX		
R	WPI; 2002-292408/33.		
D	DR		
D	N-PSDB; ABN32777.		
X	XX		
P	An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.		
X	XX		
P	Claim 20; SEQ ID NO 859; 509pp; English.		
X	XX		
C	The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention		
C	XX		
C	Sequence 309 AA;		
Qy	3 DGLWNNGTQ---TQFLFH 17		
Db	74 DGWTNDNQLOQEMADRIKH 92		
RESULT 40	AAM40322		
ID	AAM40322 standard; protein; 511 AA.		

Search completed: December 30, 2004, 16:10:01  
 Job time : 165 sec

XX  
 AC AAM40322;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 3467.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20015312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US034263.  
 XX  
 PR 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-00523117.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-0053450.  
 PR 14-SEP-2000; 2000US-0062191.  
 PR 19-OCT-2000; 2000US-0063036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PT Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 XX  
 PR Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI: 2001-44253/47.  
 DR N-PSDB; AA159478.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX  
 PS Example 6; SEQ ID NO 3467; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AAM3862-AAM4223) with nootropic,  
 CC immunosupressant and cytosatatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 XX  
 SQ Sequence 511 AA;

Query Match 45.5%; Score 45; DB 4; Length 511;  
 Best Local Similarity 47.4%; Pred. No. 2.6e-02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 3 DGLWMNNO---TQPLEH 17  
 QY |||||:|||:::  
 QY 74 DGTWNNDNQLOEQAQLRIKH 92

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Run on: December 30, 2004, 16:13:23 ; Search time 143 Seconds  
(without alignments)  
45.280 Million cell updates/sec

Title: US-10-718-321-1

Perfect score: 99  
Sequence: 1 SSDGLMNNNQTLFLEHS 18

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters:  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 150 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpa/US05\_NEW\_PUB\_pep: \*  
4: /cgn2\_6/ptodata/1/pubpa/US06\_PUBCOMB.pep: \*  
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12: /cgn2\_6/ptodata/1/pubpa/US09\_NEW\_PUB\_pep: \*  
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19: /cgn2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*  
20: /cgn2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep: \*

Pred. No. 16 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	99	100.0	359	14 US-10-188-012-17 Sequence 17, Appl
2	99	100.0	359	14 US-10-188-012-19 Sequence 19, Appl
3	99	100.0	359	14 US-10-295-27-302 Sequence 302, Appl
4	99	100.0	359	15 US-10-188-832-64 Sequence 64, Appl
5	99	100.0	364	14 US-10-188-012-25 Sequence 25, Appl
6	99	100.0	364	14 US-10-188-012-27 Sequence 27, Appl
7	99	100.0	365	14 US-10-188-012-21 Sequence 21, Appl
8	94	94.9	359	14 US-10-188-012-23 Sequence 23, Appl
9	48	48.5	981	9 US-09-991-2589-13 Sequence 13, Appl
10	47	47.5	102	15 US-10-424-599-175126 Sequence 175126, Appl
11	46	46.5	508	14 US-10-369-493-1469 Sequence 1469, Appl
12	46	46.5	16	US-10-451-467A-56 Sequence 56, Appl
13	46	46.5	545	15 US-10-389-566-1218 Sequence 1218, Appl

### SUMMARIES

Summary No.	Score	Query Match Length	DB ID	Description
1	99	100.0	359	14 US-10-188-012-17 Sequence 17, Appl
2	99	100.0	359	14 US-10-188-012-19 Sequence 19, Appl
3	99	100.0	359	14 US-10-295-27-302 Sequence 302, Appl
4	99	100.0	359	15 US-10-188-832-64 Sequence 64, Appl
5	99	100.0	364	14 US-10-188-012-25 Sequence 25, Appl
6	99	100.0	364	14 US-10-188-012-27 Sequence 27, Appl
7	99	100.0	365	14 US-10-188-012-21 Sequence 21, Appl
8	94	94.9	359	14 US-10-188-012-23 Sequence 23, Appl
9	48	48.5	981	9 US-09-991-2589-13 Sequence 13, Appl
10	47	47.5	102	15 US-10-424-599-175126 Sequence 175126, Appl
11	46	46.5	508	14 US-10-369-493-1469 Sequence 1469, Appl
12	46	46.5	16	US-10-451-467A-56 Sequence 56, Appl
13	46	46.5	545	15 US-10-389-566-1218 Sequence 1218, Appl

Summary No.	Score	Query Match Length	DB ID	Description
1	99	100.0	359	14 US-10-188-012-17 Sequence 17, Appl
2	99	100.0	359	14 US-10-188-012-19 Sequence 19, Appl
3	99	100.0	359	14 US-10-295-27-302 Sequence 302, Appl
4	99	100.0	359	15 US-10-188-832-64 Sequence 64, Appl
5	99	100.0	364	14 US-10-188-012-25 Sequence 25, Appl
6	99	100.0	364	14 US-10-188-012-27 Sequence 27, Appl
7	99	100.0	365	14 US-10-188-012-21 Sequence 21, Appl
8	94	94.9	359	14 US-10-188-012-23 Sequence 23, Appl
9	48	48.5	981	9 US-09-991-2589-13 Sequence 13, Appl
10	47	47.5	102	15 US-10-424-599-175126 Sequence 175126, Appl
11	46	46.5	508	14 US-10-369-493-1469 Sequence 1469, Appl
12	46	46.5	16	US-10-451-467A-56 Sequence 56, Appl
13	46	46.5	545	15 US-10-389-566-1218 Sequence 1218, Appl

GENERAL INFORMATION:  
 APPLICANT: McIntire, Jennifer Jones  
 APPLICANT: Umetsu, Dale T.  
 APPLICANT: Dekruyff, Rosemarie  
 APPLICANT: Kuchroo, Vijay  
 APPLICANT: Freeman, Gordon J.

TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
 Sequence 245, App  
 Sequence 246, App  
 Sequence 72863, A  
 Sequence 62190, A  
 Sequence 45949, A  
 Sequence 22409, A  
 Sequence 20045, A  
 Sequence 240616, A  
 Sequence 212481, A  
 Sequence 220754, A  
 Sequence 37854, A  
 Sequence 18823, A  
 Sequence 41661, A  
 Sequence 152589, A  
 Sequence 53310, A  
 Sequence 227847, A  
 Sequence 36719, A  
 Sequence 122654, A  
 Sequence 4, Appli  
 Sequence 15, Appli  
 Sequence 36721, A  
 Sequence 289, App  
 Sequence 32998, A  
 Sequence 10, Appli  
 Sequence 206691,  
 Sequence 207559,  
 Sequence 6691, AP  
 Sequence 2351, AP  
 Sequence 1217, AP  
 Sequence 1508, AP  
 Sequence 2319, AP  
 Sequence 70123, A  
 Sequence 73028, A  
 Sequence 51304, A  
 Sequence 1926, AP  
 Sequence 9, Appli  
 Sequence 11, Appli  
 Sequence 161, AP  
 Sequence 167129,  
 Sequence 53, Appli  
 Sequence 53, Appli  
 Sequence 34, Appli  
 Sequence 344, AP  
 Sequence 1390, AP  
 Sequence 148, AP  
 Sequence 208, AP  
 Sequence 6237, AP  
 Sequence 41570, A  
 Sequence 201446,  
 Sequence 3, Appli  
 Sequence 405, APP  
 Sequence 147295,  
 Sequence 363170  
 Sequence 350274,  
 Sequence 216289,  
 Sequence 147, APP  
 Sequence 72, APP1  
 Sequence 2191, AP  
 Sequence 72, APP1  
 Sequence 339063,  
 Sequence 204170,  
 Sequence 194265,  
 Sequence 253434,  
 Sequence 162608,

PRIOR FILING DATE: 2001-06-29  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 17  
 CURRENT FILING DATE: 2002-07-01  
 PRIORITY APPLICATION NUMBER: 60/302,344  
 LENGTH: 359  
 TYPE: PRT  
 ORGANISM: H. sapiens  
 FEATURE: VARIANT  
 NAME/KEY: VARIANT  
 LOCATION: (1)...(360)  
 OTHER INFORMATION: TIM-1 allele 1

US-10-188-012-17

Query Match 100.0%; Score 99; DB 14; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-0%; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 1 SSDGLWNNTQFLEHS 18  
 Db 264 SSDGLWNNTQFLEHS 281

RESULT 2

US-10-188-012-19

Publication 19, Application US/10188012  
 Publication No. US20030124114A1

GENERAL INFORMATION:  
 APPLICANT: McIntire, Jennifer Jones  
 APPLICANT: Umetsu, Dale T.  
 APPLICANT: Dekruyff, Rosemarie  
 APPLICANT: Kuchroo, Vijay  
 APPLICANT: Freeman, Gordon J.

TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
 Sequence 16, AP  
 Sequence 100.0%; Pred. No. 2,3e-0%; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 1 SSDGLWNNTQFLEHS 18  
 Db 264 SSDGLWNNTQFLEHS 281

US-10-188-012-19

Publication 19, Application US/10188012  
 Publication No. US20030124114A1

GENERAL INFORMATION:  
 APPLICANT: McIntire, Jennifer Jones  
 APPLICANT: Umetsu, Dale T.  
 APPLICANT: Dekruyff, Rosemarie  
 APPLICANT: Kuchroo, Vijay  
 APPLICANT: Freeman, Gordon J.

TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
 Sequence 16, AP  
 Sequence 100.0%; Pred. No. 2,3e-0%; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 1 SSDGLWNNTQFLEHS 18  
 Db 264 SSDGLWNNTQFLEHS 281

CURRENT APPLICATION NUMBER: US/10/188,012

CURRENT FILING DATE: 2002-07-01  
 PRIOR APPLICATION NUMBER: 60/302,344  
 PRIOR FILING DATE: 2001-06-29  
 NUMBER OF SEQ ID NOS: 36  
 TITLE OF INVENTION: Use Thereof  
 FILE REFERENCE: STAN-235  
 SEQ ID NO: 19  
 LENGTH: 359  
 TYPE: PRT  
 ORGANISM: H. sapiens  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (1)...(359)  
 OTHER INFORMATION: TIM-1, allele 2

US-10-188-012-19

Query Match 100.0%; Score 99; DB 14; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-0%; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 1 SSDGLWNNTQFLEHS 18  
 Db 264 SSDGLWNNTQFLEHS 281

## ALIGNMENTS

RESULT 1  
 US-10-188-012-17  
 ; Sequence 17, Application US/10188012  
 ; Publication No. US20030124114A1

RESULT 3

US-10-295-027-302  
; Sequence 302, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Heveri, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Bob Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; CURRENT FILING DATE: 2002-11-13  
; FILE REFERENCE: 018501-012500US  
; PRIOR APPLICATION NUMBER: US 10/295,027  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 302  
; LENGTH: 359  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-295-027-302  
; Query Match 100.0%; Score 99; DB 14; Length 359;  
; Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
; Matches 18; Conservative 0; Mismatches 0;  
; Indels 0; Gaps 0;  
; Qy 1 SSDGLWNNTQOLFLEHS 18  
; Db 264 SSDGLWNNTQOLFLEHS 281  
; RESULT 5  
; Sequence 25, Application US/10188012  
; Publication No. US20030124114A1  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruff, Rosemarie  
; APPLICANT: Kuchroo, Vijay  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(364)  
; OTHER INFORMATION: TIM-1 allele 5  
; US-10-188-012-25  
; Query Match 100.0%; Score 99; DB 14; Length 364;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
; Matches 18; Conservative 0; Mismatches 0;  
; Indels 0; Gaps 0;  
; Qy 1 SSDGLWNNTQOLFLEHS 18  
; Db 269 SSDGLWNNTQOLFLEHS 286  
; RESULT 6  
; Sequence 27, Application US/10188012  
; Publication No. US20030124114A1  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruff, Rosemarie  
; APPLICANT: Kuchroo, Vijay  
; APPLICANT: Freeman, Gordon J.

RESULT 4  
; Sequence 64, Application US/10188032  
; Publication No. US20040076955A1  
; GENERAL INFORMATION:  
; APPLICANT: Mack, David H.  
; APPLICANT: Bob Biotechnology, Inc.  
; APPLICANT: Aziz, Natasha  
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions  
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder  
; FILE REFERENCE: 018501-002330US  
; CURRENT APPLICATION NUMBER: US/10/188,832  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US 60/302,814  
; PRIOR FILING DATE: 2001-07-03

; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; SEQ ID NO: 27  
; LENGTH: 364  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 27  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; LOCATION: (1)..(364)  
; OTHER INFORMATION: TIM-1, allele 6  
; US-10-188-012-27  
; Query Match 100.0%; Score 99; DB 14; Length 364;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-07; Mismatches 0; Indels 0; Gaps 0;  
; Matches 18; Conservative 0; Name/Key: VARIANT  
; Qy 1 SSDGGLWNNTQOLFLEHS 18  
; Db 269 SSDGGLWNNTQOLFLEHS 286  
; RESULT 7  
; US-10-188-012-21  
; Sequence 21, Application US/10188012  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruyff, Rosemarie  
; APPLICANT: Kuchroo, Vijay  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; PRIOR FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 21  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; LOCATION: (1)..(365)  
; OTHER INFORMATION: TIM-1, allele 3  
; US-10-188-012-21  
; Query Match 100.0%; Score 99; DB 14; Length 365;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-07; Mismatches 0; Indels 0; Gaps 0;  
; Matches 18; Conservative 0; Name/Key: VARIANT  
; Qy 1 SSDGGLWNNTQOLFLEHS 18  
; Db 270 SSDGGLWNNTQOLFLEHS 287  
; RESULT 8  
; US-10-188-012-23  
; Sequence 23, Application US/10188012  
; Publication No. US20030124114A1  
; GENERAL INFORMATION:  
; APPLICANT: McIntire, Jennifer Jones  
; APPLICANT: Umetsu, Dale T.  
; APPLICANT: Dekruyff, Rosemarie  
; APPLICANT: Freeman, Gordon J.  
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: STAN-235  
; CURRENT APPLICATION NUMBER: US/10/188,012  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/302,344  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 23  
; LENGTH: 359  
; TYPE: PRT  
; ORGANISM: H. sapiens  
; FEATURE:  
; LOCATION: (1)..(359)  
; OTHER INFORMATION: TIM-1, allele 4  
; US-10-188-012-23  
; Query Match 94.9%; Score 94; DB 14; Length 359;  
; Best Local Similarity 94.4%; Pred. No. 1.5e-06; Mismatches 0; Indels 0; Gaps 0;  
; Matches 17; Conservative 1; Name/Key: VARIANT  
; Qy 1 SSDGGLWNNTQOLFLEHS 18  
; Db 264 SSDGGLWNNTQOLFLEHS 281  
; RESULT 9  
; US-09-991-258-13  
; Sequence 13, Application US/09991258  
; GENERAL INFORMATION:  
; APPLICANT: Olmsted, Robert  
; APPLICANT: Keith, Paula  
; APPLICANT: Driga, Sergey  
; APPLICANT: Cailey, Ian  
; APPLICANT: Maughan, Maureen  
; APPLICANT: Johnston, Robert  
; APPLICANT: Davis, Nancy  
; APPLICANT: Swanstrom, Ronald  
; TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE IN  
; TITLE OF INVENTION: VACCINES  
; FILE REFERENCE: 0113-0001U3  
; CURRENT APPLICATION NUMBER: US/09/991,258  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 09/902,537  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/216,995  
; PRIOR FILING DATE: 2000-07-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 13  
; LENGTH: 981  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1= US-09-991-258-13  
; Query Match 48.5%; Score 48; DB 9; Length 981;  
; Best Local Similarity 50.0%; Pred. No. 83; Mismatches 5; Indels 0; Gaps 0;  
; Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1= US-09-991-258-13  
; Qy 1 SSDGGLWNNTQOLFLEHS 16  
; Db 489 SSDGGLWNNTQOLFLEHS 504

RESULT 10  
US-10-24-599-175126  
Sequence 175126, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: JAB-1667  
FILE NUMBER: 38-21(5323)B  
FILE REFERENCE: 38-21(5323)B  
PRIORITY NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 175126  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129157C.1.pep  
US-10-424-599-175126

Query Match Score 47; DB 15; Length 102;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SDGGLWNNTQQLFL 15  
Db 79 STGQIWINWTHLU 93

RESULT 11  
US-10-369-1469  
Sequence 1469, Application US/10369493  
Publication No. US20030235675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinklin, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-0(5205)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 1469  
LENGTH: 508  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae

US-10-369-1469

Query Match Score 46.5%; DB 14; Length 508;  
Best Local Similarity 63.6%; Pred. No. 86;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 WANNQTLFL 16  
Db 160 WNNNNSMFL 170

RESULT 13  
US-10-389-566-1218  
Sequence 1218, Application US/10389566  
Publication No. US20040025202A1  
GENERAL INFORMATION:  
APPLICANT: Monantco Technology, LLC  
APPLICANT: Laurie, Cathy C.  
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants FILE REFERENCE: 38-77(5200)D  
CURRENT APPLICATION NUMBER: US/10/389,566  
CURRENT FILING DATE: 2003-03-31  
PRIOR APPLICATION NUMBER: US 60/365,301  
PRIOR FILING DATE: 2002-03-15  
PRIOR APPLICATION NUMBER: US 60/391,786  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/392,018  
PRIOR FILING DATE: 2002-06-26  
NUMBER OF SEQ ID NOS: 2459  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1218  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Solanum tuberosum

US-10-389-566-1218

Query Match Score 46.5%; DB 15; Length 545;  
Best Local Similarity 57.1%; Pred. No. 92;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 DGLWNNTQQLFL 16  
Db 324 DGTWNSEYQQFL 337

RESULT 14  
US-10-437-963-163657  
Sequence 163657, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei

RESULT 12  
US-10-451-467A-56  
Sequence 56, Application US/10451467A  
Publication No. US2004016140A1  
GENERAL INFORMATION:  
APPLICANT: CONTRERAS, ROLAND HENRI  
APPLICANT: EBERHARD, INES  
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS

APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barbazuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement  
 CURRENT APPLICATION NUMBER: US10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO 153221  
 LENGTH: 384  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62632C.1.pep  
 ; US-10-437-963-163657

Query Match 46.0%; Score 45.5; DB 16; Length 384;  
 Best Local Similarity 61.1%; Pred. No. 77;  
 Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SDG---LWNNTQTLFL 15  
 Db 168 SDDGSVKLWNNTQTLFL 185

RESULT 15  
 US-10-437-963-163658  
 Sequence 163658, Application US/10437963  
 Publication No. US20040123343A1  
 GENERAL INFORMATION:  
 APPLICANT: Li, Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yinhua  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Wu, Wei  
 APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barbazuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(53221)B  
 CURRENT APPLICATION NUMBER: US10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO 163658  
 LENGTH: 770  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 NAME/KEY: unsure  
 LOCATION: (1)..(770)  
 OTHER INFORMATION: unsure at all xaa locations  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_62633C.1.pep  
 ; US-10-437-963-163658

Query Match 46.0%; Score 45.5; DB 16; Length 770;  
 Best Local Similarity 61.1%; Pred. No. 1.6e-02;  
 Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SDG---LWNNTQTLFL 15  
 Db 554 SDDGSVKLWNNTQTLFL 571

RESULT 16  
 US-10-156-761-9511  
 Sequence 9511, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHITAKA  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 24-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO 9511  
 LENGTH: 273  
 TYPE: PRT  
 ORGANISM: Streptomyces avermitilis  
 ; US-10-156-761-9511

Query Match 45.5%; Score 45; DB 14; Length 273;  
 Best Local Similarity 56.2%; Pred. No. 64;  
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SDGWNNTQTLFLH 17  
 Db 126 SGGEWGRGLFOLPFLH 141

RESULT 17  
 US-10-282-122A-485-22  
 Sequence 48522, Application US/10282122A  
 Publication No. US20040029129A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zveckin, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELTRIA-034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 601206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 601207,727  
 PRIOR FILING DATE: 2000-05-25  
 PRIOR APPLICATION NUMBER: 601230,335  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 601230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 601242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 601253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 601257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 601267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 601269,308  
 PRIOR FILING DATE: 2001-02-15  
 Remaining prior application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 48522  
; LENGTH: 687  
; TYPE: PRT  
; ORGANISM: *Bacteroides fragilis*  
; US-10-882-12A-45522

Query Match 45.5%; Score 45; DB 15; Length 687;  
Best local Similarity 54.5%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DGLWNNTQQL 13  
Db 519 EGWMSNDQTEL 529

RESULT 18  
US-09-934-070-15  
Sequence 15, Application US/09934070  
Publication No. US20030092004A1  
GENERAL INFORMATION:  
APPLICANT: Lipton, Stuart A.  
APPLICANT: Zhang, Dongxian  
APPLICANT: Chatterton, Jon B.  
APPLICANT: Awobuluyi, Marc  
APPLICANT: Sevarino, Kevin A.  
TITLE OF INVENTION: EXCITATORY GLYCINE RECEPTORS AND METHODS  
FILE REFERENCE: P-LJ 4900  
CURRENT APPLICATION NUMBER: US/09/934,070  
CURRENT FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

US-09-934-070-15

Query Match 45.5%; Score 45; DB 10; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQPLEH 17  
Db 1174 NEDGLPNNDQYKLYAKH 1190

RESULT 19  
US-09-932-011-1  
Sequence 1, Application US/09922011  
Publication No. US20030099331A1  
GENERAL INFORMATION:  
APPLICANT: CIS Biotech, Inc.  
APPLICANT: Damboina, Svetlana  
TITLE OF INVENTION: Rapid multiple panel of biomarkers in laboratory blood tests for  
TITLE OF INVENTION: Rapid multiple panel of biomarkers in laboratory blood tests for  
FILE REFERENCE: 08805.103001  
CURRENT APPLICATION NUMBER: US/09/932,011  
CURRENT FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 1  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *homo sapiens*

US-09-932-011-1

Query Match 45.5%; Score 45; DB 10; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQPLEH 17  
Db 1174 NEDGLPNNDQYKLYAKH 1190

---

RESULT 20  
US-10-222-772-15  
Sequence 15, Application US/10222772  
Publication No. US20040013500A1  
GENERAL INFORMATION:  
APPLICANT: Lipton, Stuart A.  
APPLICANT: Zhang, Dongxian  
APPLICANT: Chatterton, Jon B.  
APPLICANT: Awobuluyi, Marc  
APPLICANT: Sevarino, Kevin A.  
TITLE OF INVENTION: EXCITATORY GLYCINE RECEPTORS AND METHODS  
FILE REFERENCE: P-LJ 5338  
CURRENT APPLICATION NUMBER: US/09/934,070  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 1464  
TYPE: PRT  
ORGANISM: *Rattus sp.*

US-10-222-772-15

Query Match 45.5%; Score 45; DB 15; Length 1464;  
Best Local Similarity 47.1%; Pred. No. 3.8e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQPLEH 17  
Db 1174 NEDGLPNNDQYKLYAKH 1190

RESULT 21  
US-10-739-930-9140  
Sequence 9340, Application US/10739930  
Publication No. US20040216190A1  
GENERAL INFORMATION:  
APPLICANT: Kovacic, David K.  
TITLE OF INVENTION: PLANTS AND USRS THEREOF FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(5337)B  
CURRENT APPLICATION NUMBER: US/10/739,930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
SEQ ID NO 9140  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE: Glycine max  
OTHER INFORMATION: Clone ID: GLYMA-23APR03-C4363\_4.p  
US-10-739-930-9140

Query Match 44.4%; Score 44; DB 17; Length 243;  
Best Local Similarity 52.9%; Pred. No. 82; Mismatches 5; Indels 2; Gaps 1;  
Matches 9; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 2 SDGLWNNTQPLEHS 18  
Db 2 ADGYNRQOA-FLPHS 16

RESULT 22  
US-10-424-599-173377  
Sequence 173377, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Cao Yongwei

RESULT 23  
US-10-282-122A-57369  
; Sequence 5736, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haeselbeck, Robert  
; APPLICANT: Ohlsen, Karin  
; APPLICANT: Zukind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trewick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.054A  
; CURRENT APPLICATION NUMBER: US1101282,122A  
; PRIOR APPLICATION NUMBER: 6/0191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 6/0206,849  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 6/0207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 6/0230,335  
; PRIOR FILING DATE: 2000-05-06  
; PRIOR APPLICATION NUMBER: 6/0230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 6/0242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 6/0253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 6/0257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 6/0267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 6/0269,308  
; PRIOR FILING DATE: 2001-03-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 76514  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57369  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
; US-10-282-122A-57369

RESULT 24  
US-10-369-493-3911  
; Sequence 3911, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 3911  
; LENGTH: 539  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(539)  
; OTHER INFORMATION: unsure at all Xaa locations  
; US-10-369-493-3911

RESULT 25  
US-09-826-509-517  
; Sequence 509, Application US/09826509  
; Publication No. US20030204073A1  
; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G  
; TITLE OF INVENTION: Protein-Coupled Receptors  
; FILE REFERENCE: ARRN-207  
; CURRENT APPLICATION NUMBER: US/09/826,509  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 6/0195,747  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 517  
; LENGTH: 590  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-826-509-517

Query Match 44.4%; Score 44; DB 15; Length 432;  
Best Local Similarity 63.6%; Pred. No. 1.5e+02; Mismatches 11; Indels 0; Gaps 0;  
Matches 7; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 5 LWNNNQDQLPFL 15  
Db 72 LWNSNKEDLFL 82

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQTLFLEHS 18  
Db 332 SSSDSWNNDAAASLENS 349

RESULT 26  
US-10-225-567A-440  
; Sequence 440, Application US/10225567A  
; Publication No. US200301013798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: 6/0257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 440  
; LENGTH: 590  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-440

Query Match 44.4%; Score 44; DB 14; Length 590;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQTLFLEHS 18  
Db 332 SSSDSWNNDAAASLENS 349

RESULT 27  
US-10-352-684A-40  
; Sequence 40, Application US/10352684A  
; Publication No. US20030215452A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Welch, Nadine S.  
; APPLICANT: Kelly, Louise M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,  
; TITLE OF INVENTION: 15513, 17822, 30, 5677, 194, 14393, 2059, 7365, 12212,  
; TITLE OF INVENTION: 1981, 261, 12456, 270, 1410, 137, 1871, 13051, 1847, 1849,  
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES  
; FILE REFERENCE: MPI02-0191RN0WM  
; CURRENT APPLICATION NUMBER: US/10/352,684A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: US 60/354,333  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: US 60/360,258  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/364,476  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/375,626  
; PRIOR FILING DATE: 2002-04-26  
; PRIOR APPLICATION NUMBER: US 60/386,494  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/390,965  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US 60/392,480  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 60/394,128  
; PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/399,783  
PRIOR FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US 60/403,221  
PRIOR FILING DATE: 2002-08-13  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 40  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-352-684A-40

Query Match 44.4%; Score 44; DB 14; Length 590;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQTLFLEHS 18  
Db 332 SSSDSWNNDAAASLENS 349

RESULT 28  
US-10-029-009-11  
; Sequence 11, Application US/10029009  
; Publication No. US20020164617A1  
; GENERAL INFORMATION:  
; APPLICANT: Felisch, Jason S.  
; APPLICANT: Annis, David Allen  
; APPLICANT: Kalghatgi, Krishna  
; APPLICANT: Nash, Haw M.  
; TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins  
; CURRENT APPLICATION NUMBER: US/10/029,009  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/258,970  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 608  
; TYPE: PRT  
; ORGANISM: Rat  
US-10-029-009-11

Query Match 44.4%; Score 44; DB 13; Length 608;  
Best Local Similarity 50.0%; Pred. No. 2.0e+02; Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQTLFLEHS 18  
Db 331 SSSDSWNNDAAASLENS 348

RESULT 29  
US-10-029-009-23  
; Sequence 23, Application US/10029009  
; Publication No. US20020164617A1  
; GENERAL INFORMATION:  
; APPLICANT: Felisch, Jason S.  
; APPLICANT: Annis, David Allen  
; APPLICANT: Kalghatgi, Krishna  
; APPLICANT: Nash, Haw M.  
; TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins  
; CURRENT APPLICATION NUMBER: US/10/029,009  
; FILE REFERENCE: 11025.173 US2  
; CURRENT APPLICATION NUMBER: US/10/029,009  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/258,970  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 626





CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO: 174682  
 LENGTH: 684  
 TYPE: PRT  
 ORGANISM: *Oryza sativa*  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_725C.1.pep  
 US-10-437-963-174682

Query Match 43.4%; Score 43; DB 16; Length 684;  
 Best Local Similarity 63.6%; Pred. No. 3.5e-02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LWNNTNQTL 15  
 Db 431 LWSNNKELFL 441

RESULT 38  
 US-10-156-761-9394  
 Sequence 9394, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHIOUKI  
 APPLICANT: HATTORI, MASAMIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-06-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 9394  
 LENGTH: 973  
 TYPE: PRT  
 ORGANISM: *Streptomyces avermitilis*  
 US-10-156-761-9394

Query Match 43.4%; Score 43; DB 14; Length 973;  
 Best Local Similarity 63.6%; Pred. No. 5.1e-02; Mismatches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DGLMNNTNQTL 13  
 Db 872 DGMMNNYQDSL 882

RESULT 39  
 US-10-424-599-265756  
 Sequence 265756, Application US/10424599  
 Publication No. US20040031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 3-21(5222)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 369326  
 SEQ ID NO: 367358  
 LENGTH: 50  
 TYPE: PRT  
 ORGANISM: *Zea mays*  
 FEATURE:  
 OTHER INFORMATION: Clone ID: MRT4577\_98200C.1.pep  
 US-10-425-115-367358

Query Match 42.4%; Score 42; DB 17; Length 50;  
 Best Local Similarity 42.9%; Pred. No. 32; Mismatches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 5 LWNNTNQTLFLEHS 18  
 Db 9 VWSNHRVGFLOHS 22

Search completed: December 30, 2004, 16:25:32  
 Job time : 147 secs

FILE REFERENCE: 38-21(5322)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO: 265756  
 LENGTH: 42  
 TYPE: PRT

GenCore version 5.1.5										
Run on: Copyright (c) 1993 - 2004 CompuGen Ltd.										
Om protein - protein search, using SW model										
Title: US-10-718-321-1									27	
Perfect score: 99									31	
Sequence: 1 SSDGLWNNNQTLQFLERS 18									31.3	
Scoring table: BLOSUM62									28	
Gapext 10.0 , Gapext: 0.5									29	
Searched: 2002273 seqs, 358729399 residues									30	
Total number of hits satisfying chosen parameters: 686242									31	
Minimum DB seq length: 0									31.3	
Maximum DB seq length: 20									31	
Post-processing: Minimum Match 0%									32	
Maximum Match 100%									33	
Listing first 150 summaries									34	
Database : A_Geneseq_23Seq04:*									35	
1: geneseqP1980s:*									36	
2: geneseqP1900s:*									37	
3: geneseqP2000s:*									38	
4: geneseqP2010s:*									39	
5: geneseqP2002s:*									39	
6: geneseqP2003s:*									39	
7: geneseqP2004s:*									39	
8: geneseqP2004s:*									39	
Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									40	
SUMMARIES										
Result No.	Score	Query Length	DB ID	Description						
1	99	100.0	18	AAC026687	Aac26687	Human_KIM	Aac26673	Monoclonal	20	
2	99	100.0	18	AAC026673	Aac26685	Human_KIM	Aac26685	Human_KIM	20	
3	53.5	18	6	AAC026686	Aac026688	Human_KIM	Aac026688	Human_KIM	20	
4	46	46.5	18	AAC026688	ADH35129	Complement	ADH35129	N-linked	20	
5	35.4	18	8	ADH35129	ADH35000	Chemokine	ADH35000	Chemokine	20	
6	35.4	19	19	ADH35000	ADH36109	Abu13471	Abu13471	Zona_pell	20	
7	34.3	12	7	ADH36109	ADG78515	Abp83017	Abp83017	G_protein	20	
8	34	34.3	19	6	ABU13471	Adel1136	Adel1136	Antigenic	20	
9	34	34.3	20	5	ABG80887	Abp80887	Abp80887	Human_esl	20	
10	33.3	18	8	ADH36109	ADG78515	Abp14120	Abp14120	Novel_hum	20	
11	33	20	5	ADH36109	ADG78515	Abu13471	Abu13471	Zona_pell	20	
12	33	20	5	ADH36109	ADG78515	Abp80887	Abp80887	Novel_hum	20	
13	33.3	20	8	ADG78515	ADG78515	Abp14120	Abp14120	Novel_hum	20	
14	33	33.3	20	8	ADG78515	ADG78515	Abp80887	Abp80887	Novel_hum	20
15	32.3	12	9	ADG78515	ADG78515	Abp80887	Abp80887	Novel_hum	20	
16	32	32.3	18	2	AAW07984	AAW07984	AAW07984	FIV_princ	20	
17	32	32.3	19	2	AAW07984	AAW07984	AAW07984	FIV_princ	20	
18	31.3	15	4	AAW07984	AAW07984	AAW07984	AAW07984	FIV_princ	20	
19	31	31.3	15	8	ADJ38603	ADJ38603	ADJ38603	HSV-4_BFL	20	
20	31	31.3	15	8	ADJ38603	ADJ38603	ADJ38603	HSV-4_BFL	20	
21	31	31.3	15	8	ADJ25941	ADJ25941	ADJ25941	Synthetic	20	
22	31	31.3	15	8	ADJ25933	ADJ25933	ADJ25933	Synthetic	20	
23	31	31.3	15	8	ADJ25932	ADJ25932	ADJ25932	Synthetic	20	
24	31	31.3	15	8	ADJ25940	ADJ25940	ADJ25940	Synthetic	20	
25	31	31.3	17	5	ADM50838	ADM50838	ADM50838	HCV_E2_re	20	

99 29 29.3 17 4 AAV72451 MAGB-1/3-  
100 29 29.3 19 2 AAR28864 Sequence  
101 29 29.3 20 6 ABR5459 Group A S  
102 29 29.3 20 8 ADH37233 Epstein B  
103 29 29.3 20 8 ADH31234 Hepatitis B  
104 29 29.3 20 8 ADM2217 Hepatitis B  
105 28.5 28.8 15 8 ADP2555 Plasmodium  
106 28 28.3 8 2 AAW5980 Interleukin  
107 28 28.3 8 2 AAW6619 Random peptide  
108 28 28.3 8 2 AAW58094 Peptide S  
109 28 28.3 8 2 AAY09742 Interleukin  
110 28 28.3 8 3 AAB1545 VIP-mimetic  
111 28 28.3 8 5 ABB71147 VIP mimetic  
112 28 28.3 8 7 ADJ73301 Vasoactive  
113 28 28.3 8 7 ADJ55935 CH1 delet  
114 28 28.3 9 2 AAW39838 Light chain  
115 28 28.3 9 2 AAW39839 Human can  
116 28 28.3 9 6 ABR1854 Human can  
117 28 28.3 9 6 ABR12626 Human can  
118 28 28.3 9 6 ABR13035 Human can  
119 28 28.3 9 6 ABR12250 Human can  
120 28 28.3 10 6 ABR212361 Human can  
121 28 28.3 10 6 ABR11883 Human can  
122 28 28.3 10 6 ABR12318 Human can  
123 28 28.3 10 6 ABR12482 Human can  
124 28 28.3 10 6 ABR12695 Human can  
125 28 28.3 10 6 ABR11909 Human can  
126 28 28.3 11 2 AAR57750 Ad5 fibre  
127 28 28.3 12 2 AAW07638 P. suis 1  
128 28 28.3 12 2 AAW68895 Peptide o  
129 28 28.3 12 2 AAW60549 Oligopeptid  
130 28 28.3 12 2 AAW5091 Peptide S  
131 28 28.3 12 2 AAW58090 Peptide S  
132 28 28.3 12 4 AAB50187 Mycobacteria  
133 28 28.3 13 5 AAY94566 Vasoactive  
134 28 28.3 13 5 AAY22277 Human int.  
135 28 28.3 13 5 ADG66480 Human G-P  
136 28 28.3 13 6 ADG5580 Human IL  
137 28 28.3 13 7 ADJ89122 Human int.  
138 28 28.3 13 7 AAE33009 Human her.  
139 28 28.3 14 2 AAR69361 Stearoyl-  
140 28 28.3 14 3 AAY94563 Vasoactive  
141 28 28.3 14 4 AAG98115 Human SNP  
142 28 28.3 14 5 ABG34903 Human G-P  
143 28 28.3 14 5 ABJ00739 B Lymphoc  
144 28 28.3 14 5 ABJ00775 B Lymphoc  
145 28 28.3 14 5 ABJ00765 B Lymphoc  
146 28 28.3 14 5 ABG33636 B Lymphoc  
147 28 28.3 14 5 ABG33626 B Lymphoc  
148 28 28.3 14 6 ADA03332 Angiotensin  
149 28 28.3 14 6 ADA03332 Angiotensin  
150 28 28.3 14 6 ABR56702 Angiotensin

**RESULT 1**  
**AAQ26687 ID AAQ26687 standard; peptide; 18 AA.**  
**XX AC AAQ26687;**  
**XX DT 20-MAR-2003 (first entry)**

**XX DR Human KIM-1 mucin domain related peptide, SEQ ID No 15.**  
**XX KW Cytostatic; gene therapy; antibody; antigen; antigen-binding; proteinolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer.**  
**XX OS Synthetic.**

**ALIGNMENTS**

Aau72451 MAGB-1/3-  
Aar4864 Sequence  
Abs52459 Group A S  
Adh37233 Epstein B  
Adh31234 Epstein B  
Adm2217 Hepatitis B  
Adp26565 Plasmodium  
Aaw5980 Interleukin  
Aaw6619 Random peptide  
Aaw58094 Peptide S  
Aay09742 Interleukin  
Aab1545 VIP-mimetic  
Abt73147 VIP mimetic  
Adj73301 Vasoactive  
Aab13035 Human can  
Aab12250 Human can  
Abt12361 Human can  
Abt11883 Human can  
Abt12318 Human can  
Abt12482 Human can  
Abt12695 Human can  
Abt11909 Human can  
Aar57750 Ad5 fibre  
Aaw07638 P. suis 1  
Aaw8895 Peptide o  
Aaw60549 Oligopeptid  
Aaw5091 Peptide S  
Aaw8090 Peptide S  
Aab50187 Mycobacteria  
Aay94566 Vasoactive  
Aay22277 Human int.  
Adg66480 B. amylool  
Adg5580 Human IL  
Aae33009 Human int.  
Adh89122 Human her.  
Aar69361 Stearoyl-  
Aay94563 Vasoactive  
Aag98115 Human SNP  
Abg34903 Human G-P  
Abj00739 B Lymphoc  
Abj00775 B Lymphoc  
Abj00765 B Lymphoc  
Abg33636 B Lymphoc  
Abg33626 B Lymphoc  
Abg33600 B Lymphoc  
Ada03332 Angiotensin  
Abr56702 Angiotensin

**RESULT 2**  
ABG34903 Human G-P  
ABJ00739 B Lymphoc  
ABJ00775 B Lymphoc  
ABJ00765 B Lymphoc  
ABG33636 B Lymphoc  
ABg33626 B Lymphoc  
ABg33600 B Lymphoc  
Ada03332 Angiotensin  
Abr56702 Angiotensin

Query Match 100.0%; Score 99; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSDGLWNWNQNTQPLEHS 18  
Db 1 SSDGLWNWNQNTQPLEHS 18

**RESULT 3**  
AAQ26673 ID AAQ26673 standard; peptide; 18 AA.  
XX AC AAQ26673;  
XX DT 20-MAR-2003 (first entry)  
DE Monoclonal antibody binding epitope, SEQ ID No 1.  
XX CYTOSTATIC; gene therapy; antibody; antigen; antigen-binding; KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1; renal disease; injury; renal cancer; binding epitope.  
XX OS Homo sapiens.  
XX PN WO20029920-A1.  
XX PD 12-DEC-2002.  
XX PF 31-MAY-2002; 2002WO-US017402.  
XX PR 01-JUN-2001; 2001US-0295449P.  
PR 04-JUN-2001; 2001US-0295907P.  
PA (BIOJ ) BIOPHARM INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
XX PI Baillie V, Bonventre J;

WO20029920-A1.  
PN  
XX  
PD 12-DEC-2002.  
PR 04-JUN-2001; 2001US-0295907P.  
XX  
PA (BIOJ ) BIOPHARM INC.  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Baillie V, Bonventre J;

DR WPI; 2003-156845/15.  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX Claim 4; Page 25; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC polypeptide. The antibody is also useful for inhibiting shedding of the KIM-1  
 XX Sequence 18 AA;

Query Match 100.0%; Score 99; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-08; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 1 SSDGLWNNNOTQLEHS 18  
 Db 1 SSDGLWNNNOTQLEHS 18

RESULT 3  
 A026585  
 ID A026686 standard; peptide; 18 AA.  
 XX  
 AC A026685;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX Human KIM-1 mucin domain related peptide, SEQ ID No 14.  
 DE Human KIM-1 mucin domain related peptide, SEQ ID No 14.  
 XX  
 KW Cyrostatic; gene therapy; antibody; antigen; antigen-binding;  
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
 KW renal disease; injury; renal cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO20029920-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PR 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.  
 XX  
 PR 04-JUN-2001; 2001US-0295907P.  
 XX  
 PA (BIOJ ) BIOPEN INC.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PT Bailly V, Bonventre J,  
 XX  
 DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Disclosure; Fig 1A; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related  
 CC peptide of the invention  
 XX Sequence 18 AA;

Query Match 53.5%; Score 53; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 1 SSDGLWNN 9  
 Db 10 SSDGLWNN 18

RESULT 4  
 A026688  
 ID A026688 standard; peptide; 18 AA.  
 XX  
 AC A026688;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX Human KIM-1 mucin domain related peptide, SEQ ID No 16.  
 DE Human KIM-1 mucin domain related peptide, SEQ ID No 16.  
 XX  
 KW Cyrostatic; gene therapy; antibody; antigen; antigen-binding;  
 KW proteolytic release; inhibitor; kidney injury molecule-1; KIM-1;  
 KW renal disease; injury; renal cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO20029920-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PR 31-MAY-2002; 2002WO-US017402.  
 XX  
 PR 01-JUN-2001; 2001US-0295449P.  
 XX  
 PR 04-JUN-2001; 2001US-0295907P.  
 XX  
 PA (BIOJ ) BIOPEN INC.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PT Bailly V, Bonventre J,  
 XX  
 DR WPI; 2003-156845/15.  
 XX  
 PT New antibody, antibody derivative or antigen-binding polypeptide that  
 PT inhibits proteolytic release of a soluble kidney injury molecule-1  
 PT polypeptide, useful for treating or preventing renal disease or injury,  
 PT e.g. renal cancer.  
 XX  
 PS Disclosure; Fig 1A; 42pp; English.

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1  
 CC polypeptide. This sequence represents a human KIM-1 mucin domain related  
 CC peptide of the invention  
 XX Sequence 18 AA;

Query Match 46.5%; Score 46; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OQ 10 QTOFLLEHS 18  
 Db 1 QTOFLLEHS 9

CC The invention relates to a novel antibody, antibody derivative or antigen  
 CC -binding polypeptide that inhibits proteolytic release of a soluble  
 CC kidney injury molecule-1 (KIM-1) polypeptide from KIM-1-expressing cells.  
 CC The antibody, antibody derivative or antigen-binding polypeptide is  
 CC useful for treating or preventing renal disease or injury, e.g. renal  
 CC cancer. The antibody is also useful for inhibiting shedding of the KIM-1

RESULT 5  
 ADH35129  
 ID ADH35129 standard; peptide; 18 AA.  
 XX  
 XX  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Complement c4 glycopeptide SEQ ID NO:188.  
 KW identification; quantification; glycopolyptide; glycopeptide;  
 KW differential glycosylation; cancer; glycoprotein; characterisation;  
 KW diagnostic marker; solid support; glycosylated polypeptide;  
 KW diagnostic biomarker; immunotherapy; drug development; toxicology;  
 KW drug targeting.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003102018-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PR 03-JUN-2003; 2003WO-US017635.  
 XX  
 PR 03-JUN-2002; 2002US-0385707P.  
 PR 09-MAY-2003; 2003US-0469361P.  
 XX  
 PA (SYST-) INST SYSTEMS BIOLOGY.  
 XX  
 PT Aebersold RH, Zhang H;  
 XX  
 DR WPI; 2004-081931/08.  
 XX  
 PT Identifying and quantifying glycopolyptides in sample by derivatizing  
 PT glycopolyptides, immobilizing and quantifying released glycopeptide  
 PT fragments.  
 XX  
 PS Example 6; SEQ ID NO 188; 162pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying and  
 CC quantifying glycopolyptides (I) in a sample. M1 comprises derivatising  
 CC (I), immobilising the derivatised (I), cleaving the immobilised (I),  
 CC labelling the immobilised glycopeptide fragments (II) with an isotope  
 CC tag, releasing (III) from the solid support, analysing the released (III)  
 CC using mass spectrometry, identifying a released (III) and quantifying the  
 CC amount of (II). The method alternatively comprises: (a) immobilising (I)  
 CC to a solid support; (b) cleaving the immobilised (I); (c) labelling the  
 CC immobilised glycopeptides (III) with an isotope tag; and/or (c) releasing  
 CC (III) from the solid support; and (d) analysing the released (III). Also  
 CC described: (1) immobilising (I) from a test sample or control sample to  
 CC comprising: (a) immobilising (I) from a test sample or control sample to  
 CC first solid support or second solid support respectively; (b) cleaving  
 CC the immobilised (I); (c) labelling the immobilised (III) on the first and  
 CC second supports with differential isotope tags on the respective supports  
 CC ; (d) releasing (III) from the solid support; (e) analysing (III); and  
 CC (f) identifying one or more glycosylated polypeptides having differential  
 CC glycosylation between the test sample and the control sample; and (2) a  
 CC kit comprising a hydrazide resin, periodate and a pair of differentially  
 CC labelled isotope tags. (M1) is useful for identifying and quantifying (I)  
 CC in a sample and for identifying diagnostic marker for a disease such as  
 CC cancer. (M1) is useful for determining the sites of glycosylation, in the  
 CC determining changes in the abundance of glycoproteins and changes in the  
 CC state of glycosylation at individual glycosylation sites on those  
 CC glycoproteins that occur in response to perturbations of biological  
 CC systems and organisms in health and disease. (M1) is also useful for  
 CC purifying glycosylated proteins or peptides and for isolating and  
 CC identifying glycoproteins from the cell membrane or body fluids to  
 CC determine specific glycoprotein changes related to certain disease states  
 CC or cancer. (M1) is also useful for identifying, selecting and  
 CC characterising subgroups of carbohydrates and characterisation of  
 CC diagnostic biomarkers, immunotherapy and to evaluate the effectiveness of  
 CC drugs during development, optimal dosing, toxicology, drug targeting and  
 CC related therapeutic applications. The present Sequence represents a  
 CC glycopeptide which is used in an example from the present invention.

Sequence 18 AA;

RESULT 6  
 ADH35000  
 ID ADH35000 standard; peptide; 19 AA.  
 XX  
 AC ADH35000;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE N-linked glycopeptide #19.  
 XX  
 PR identification; quantification; glycopolyptide; glycopeptide;  
 KW diagnostic marker; solid support; glycosylated polypeptide;  
 KW differential glycosylation; cancer; glycoprotein; characterisation;  
 KW diagnostic biomarker; immunotherapy; drug development; toxicology;  
 KW drug targeting.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003102018-A2.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PR 03-JUN-2003; 2003WO-US017635.  
 XX  
 PR 03-JUN-2002; 2002US-0385707P.  
 PR 09-MAY-2003; 2003US-0469361P.  
 XX  
 PA (SYST-) INST SYSTEMS BIOLOGY.  
 XX  
 PR WPI; 2004-081931/08.  
 XX  
 PT Identifying and quantifying glycopolyptides in sample by derivatizing  
 PT glycopolyptides, immobilizing and quantifying released glycopeptide  
 PT fragments.  
 XX  
 PS Example 15; Fig 28; 162pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying and  
 CC quantifying glycopolyptides (I) in a sample. M1 comprises derivatising  
 CC (I), immobilising the derivatised (I), cleaving the immobilised (I),  
 CC labelling the immobilised glycopeptide fragments (II) with an isotope  
 CC tag, releasing (III) from the solid support, analysing the released (III)  
 CC using mass spectrometry, identifying a released (III) and quantifying the  
 CC amount of (II). The method alternatively comprises: (a) immobilising (I)  
 CC to a solid support; (b) cleaving the immobilised (I); (c) labelling the  
 CC immobilised glycopeptides (III) with an isotope tag; and/or (c) releasing  
 CC (III) from the solid support; and (d) analysing the released (III). Also  
 CC described: (1) identifying (M2) diagnostic marker for a disease,  
 CC comprising: (a) immobilising (I) from a test sample or control sample to  
 CC a first solid support or second solid support respectively; (b) cleaving  
 CC the immobilised (I); (c) labelling the immobilised (III) on the first and  
 CC second supports with differential isotope tags on the respective supports  
 CC ; (d) releasing (III) from the solid support; (e) analysing (III); and  
 CC (f) identifying one or more glycosylated polypeptides having differential  
 CC glycosylation between the test sample and the control sample; and (2) a

CC kit comprising a hydrazide resin, periodate and a pair of differentially  
 CC labelled isotope tags. (M1) is useful for identifying and quantifying (I)  
 CC in a sample and for identifying diagnostic marker for a disease such as  
 CC cancer. (M1) is useful for determining the sites of glycosylation,  
 CC determining changes in the abundance of glycoproteins and changes in the  
 CC state of glycosylation at individual glycosylation sites on those  
 CC glycoproteins that occur in response to perturbations of biological  
 CC systems and organisms in health and disease. (M1) is also useful for  
 CC purifying glycosylated proteins or peptides and for isolating and  
 CC identifying glycoproteins from the cell membrane or body fluids to  
 CC determine specific glycoprotein changes related to certain disease states  
 CC or cancer. (M1) is also useful for identifying, selecting and  
 CC characterising subgroups of carbohydrates and characterisation of  
 CC diagnostic biomarkers, immunotherapy and to evaluate the effectiveness of  
 CC drugs during development, optimal dosing, toxicology, drug targeting and  
 CC related therapeutic applications. The present sequence represents an N-  
 CC linked glycopeptide which is used in an example from the present  
 CC invention.

XX Sequence 19 AA:  
 SQ Query Match 35.4%; Score 35; DB 8; Length 19;  
 CC Best local Similarity 63.6%; Pred. No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;  
 CC Matches 7; Conservative 2;  
 QY 2 SDGLWNNNQO 12  
 DB 3 SDGLESNSSTQ 13

RESULT 7  
 ADC36109  
 ID ADC36109 Standard; peptide; 12 AA.  
 XX  
 AC ADC36109;  
 XX DT 18-DEC-2003 (first entry)  
 DB Chemokine binding peptide BKR-P143.  
 XX  
 KW peptidic chemokine modulator; antiinflammatory; antiallergic;  
 KW immunosuppressive; antidiabetic; antiarthritic; dermatologic;  
 KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;  
 KW antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotropic;  
 KW cyrostatic; inflammation; allergic; immune response; autoimmune reaction;  
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
 KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;  
 KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;  
 KW hypertension; reperfusion ischaemia.  
 OS Synthetic.  
 XX  
 PN WO2003072599-A2.

XX Sequence 12 AA;

SQ

Query Match 35.4%; Score 35; DB 8; Length 12;

CC Best Local Similarity 63.6%; Pred. No. 2.6e+02; Mismatches 1; Indels 0; Gaps 0;

CC Matches 5; Conservative 1;

XX

QY 6 WNNNQO 12

DB 2 WNSNSTQ 8

XX

RESULT 8

ABU13471

ID ABU13471 Standard; peptide; 19 AA.

XX

AC ABU13471;

XX

DT 21-FEB-2003 (first entry)

XX

DE zona pellucida protein (ZP1) peptide #66.

XX

HUMAN; zona pellucida; immunogen; ZP1; sperm; contraceptive; vaccine.

XX

KW Homo sapiens.

XX

OS US6455041-B1.

XX

PR 24-SEP-2002.

XX

PP 17-NOV-1999; 99US-00441502.

XX

PR 17-NOV-1998; 98US-0108822P.

XX

PA (DUMB/) DUNBAR B S.

XX

PI Dunbar BS;

XX

WPI; 2003-089265/08.

XX

PR inducing anti-zona pellucida protein antibodies in a mammal; comprises

XX

PR administering to the mammal one or more zona pellucida peptide.

XX

PS Example 1; Col 9; 33pp; English.

XX

PS

XX  
 CC This invention relates to a novel human anti-zona pellucida protein (ZP1)  
 CC antibodies in a mammal. The method comprises administering to the mammal  
 CC one or more zona pellucida peptides shown in the specification. The  
 CC invention also discloses a method for preventing sperm binding to zona  
 CC pellucida in a mammal, this may be used as a contraceptive or to create a  
 vaccine. The method of the invention is useful for inducing antibodies to  
 CC the zona pellucida protein, thus, resulting in a contraceptive effect in  
 CC multiple mammalian species. The present sequence represents a human zona  
 CC pellucida immunogenic peptide used to generate the specific antibodies of  
 the invention  
 XX  
 SQ Sequence 19 AA:  
 Query Match 34.3%; Score 34; DB 6; Length 19;  
 Best Local Similarity 53.8%; Pred. No. 3.7e+02;  
 Matches 7; Conservative 4; Indels 0; Gaps 0;  
 Oy 1 SDGIGWNNNQQL 13  
 Db 1 SGSGIGDNYQQL 13

RESULT 9  
 ABP83017  
 ID ABP83017 standard; peptide; 20 AA.  
 XX  
 AC ABP83017;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1690.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic Peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.

PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burmer GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Claim 1; Fig 2; 523pp; English.

XX  
 CC The present invention describes antigenic peptides (1) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP8619) of 12-24 amino  
 acids. Also described: (1) an assay for the detection of a particular G  
 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or

CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 antibody against a particular GPCR, and in the production of specific  
 antibodies. The peptide and antibodies are also useful for detecting the  
 presence or absence of corresponding GPCRs. The antigenic peptides for  
 GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 regeneration-related disease, immunological-related cell proliferative  
 diseases or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 any other disorder in which GPCRs are involved. The antibodies may be  
 used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 20 AA:  
 Query Match 34.3%; Score 34; DB 6; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 SSDGLWNNN 9  
 Db 12 SSSSNWNNN 20

RESULT 10  
 ADE1136  
 ID ADB11136 standard; peptide; 18 AA.  
 XX  
 AC ADB11136;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Antigenic peptide B1-92-109 #SEQ ID 18.  
 XX  
 KW Antigenic Peptide; omega-oxidation; fatty acid; alkane; alpha;  
 KW omega-dicarboxylic acid; yeast; antibody; perfume; polymer; adhesive;  
 KW macrolide antibiotic.  
 XX  
 OS Candida tropicalis.  
 XX  
 PN WO2003089611-A2.  
 XX  
 PD 30-OCT-2003.  
 XX  
 PF 18-APR-2003; 2003WO-US012158.  
 XX  
 PR 19-APR-2002; 2002US-0074066P.  
 XX  
 PR 18-APR-2003; 2003US-00418820.  
 XX  
 PA (COGN-) COGNIS CORP.  
 XX  
 PI Zhang Y, Wilson CR;  
 XX  
 DR WPI; 2004-011692/01.  
 XX  
 PS Claim 1; SEQ ID NO 18; 66pp; English.

XX  
 CC The invention relates to antigenic peptides having any of seven specific  
 CC sequences (of 16-25 amino acids, reproduced) or their analogs,  
 CC derivatives and immunologically active fragments. They are used to raise  
 CC antibodies (Ab) that bind selectively to enzymes (II) involved in the

CC omega-oxidation of fatty acids or alkanes to alpha,omega-dicarboxylic  
 CC acids in yeast. Antigenic peptides are used to raise antibodies (Ab)  
 CC specific for yeast enzymes (II) involved in the omega-oxidation of fatty  
 CC acids or alkanes to alpha,omega-dicarboxylic acids (III). Antibodies are  
 CC used to detect/quantify (III), especially for monitoring their induction  
 CC and/or stability during oxidation to (III), e.g. for manipulating (II)  
 CC for increased yield of (III), and also to verify the effect of  
 CC modifications of yeast enzyme encoding genes. Alpha,omega-dicarboxylic  
 CC acids are useful as intermediates for perfumes, polymers, adhesives and  
 CC macrolide antibiotics. The current sequence represents an antigenic  
 CC peptide designed for recombinant antibody generation.

SQ Sequence 18 AA:

Query Match 33.3%; Score 33; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 5;  
 Matches 5; Conservative 0; Indels 0; Gaps 0;

QY 4 GLANN 8  
 Db 1 GLWNN 5

RESULT 11

ABG8087  
 ID ABG8087 standard; protein; 20 AA.

AC ABG8087;  
 XX

DT 29-NOV-2002 (first entry)

DE Human esl mutant protein E107N.

XX  
 KW Scaffold Protein; C-type lectin-like domain; CTLD; alpha-helix;  
 KW beta-strand; connecting segment; 14loop region; tetratracetin;  
 KW ligand-binding specificity; human; mouse; rat; chicken; murine; mutein.

XX  
 OS Homo sapiens.

OS Synthetic.

PN WO200248189-A2.

PD 20-JUN-2002.

XX  
 PR 13-DEC-2001; 2001WO-DK000825.

XX  
 PR 13-DEC-2000; 2000DK-00001872.

PR 28-FEB-2001; 2001US-0272098P.

PA (BORÉ-) BOREAN PHARMA AS.

PT Etzerodt M, Holter TL, Graversen NJH, Thøgersen HC;

XX  
 DR WPI: 2002-643278/69.

XX  
 PT Protein comprising a variant of model C-type lectin-like domains (CTLD),  
 PT in which alpha helices, beta-strands, connecting segments are conserved  
 PT to maintain CTLD scaffold structure, while the loop region is altered.  
 XX  
 PS Claim 1, Page 19, 168pp; English.

CC The present invention relates to a new protein with scaffold structure of  
 CC C-type lectin-like domains (CTLD). The invention comprises a variant of a  
 CC model CTLD where alpha-helices and beta-strands and connecting segments  
 CC are conserved such that scaffold structure of C-type lectin-like domains  
 CC (CTLD) is substantially maintained, while the 14loop region is altered by  
 CC amino acid substitution, deletion, insertion or their combination. The  
 CC invention is useful for preparing a library of nucleotide sequences  
 CC encoding related proteins by randomising part or all of the nucleic acid  
 CC sequence encoding the loop region of its CTLD. The artificial CTLD  
 CC protein products are preferable to antibody derivatives as each binding  
 CC site is a single structurally autonomous protein domain. When used as  
 CC components of compositions to be used for in vivo diagnostic or

CC therapeutic purposes, artificial CTLD protein products constructed on the  
 CC basis of human CTLDs are virtually identical to the corresponding natural  
 CC CTLD protein already present in the body and are therefore less  
 CC immunogenic to the patient. They also have a smaller size, and thus  
 CC provide tissue penetration and distribution, as well as shorter half life  
 CC in circulation. Since murine and human tetratracetin are identical in  
 CC structure, straightforward swapping of polypeptide segments defining  
 CC ligand-binding specificity between murine and human tetratracetin  
 CC derivatives may be achieved. The present amino acid sequence represents a  
 CC mutant protein of the invention

SQ Sequence 20 AA:

Query Match 33.3%; Score 33; DB 5; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 5.5e+02; Mismatches 4;  
 Matches 4; Conservative 3; Indels 0; Gaps 0;

QY 4 GLWNN 10  
 Db 13 GMWNDR 19

RESULT 12

ABO14120  
 ID ABO14120 Standard; peptide; 20 AA.

AC ABO14120;

DT 21-AUG-2003 (first entry)

DE Novel human secreted protein fragment #21.

XX  
 KW Human; secreted protein; cytosstatic; neuroprotective; hepatotropic;  
 KW gene therapy; cancer; liver disorder; hepatitis; neural disorder;  
 KW Alzheimer's disease.

XX  
 OS Homo sapiens.

PN US2003028003-A1.

PD 06-FEB-2003.

XX  
 PR 12-OCT-2001; 2001US-00974879.

XX  
 PR 07-NOV-1997; 97US-005490P.

PR 07-NOV-1997; 97US-006490P.

PR 07-NOV-1997; 97US-005491P.

PR 07-NOV-1997; 97US-0054912P.

PR 07-NOV-1997; 97US-006493P.

PR 07-NOV-1997; 97US-0054984P.

PR 07-NOV-1997; 97US-0054985P.

PR 07-NOV-1997; 97US-006497P.

PR 07-NOV-1997; 97US-0064988P.

PR 07-NOV-1997; 97US-0056089P.

PR 17-NOV-1997; 97US-006090P.

PR 17-NOV-1997; 97US-006094P.

PR 17-NOV-1997; 97US-005605P.

PR 17-NOV-1997; 97US-00610P.

PR 04-NOV-1998; 98WO-US023435.

PR 05-MAY-1999; 99US-00305736.

PR 13-OCT-2000; 2000US-0229893P.

PR 28-MAR-2001; 2001US-00818683.

XX  
 PA (ROSE/) ROSEN C A.

PA (FENG/) FENG P.

PA (RUBB/) RUBEN S M.

PA (EBER/) EBER R.

PA (OLSEN/) OLSEN H S.

PA (NIU/) NI J.

PA (WEI Y/ WEI Y.

PA (SOPP/) SOPPET D R.

PA (MOORE P A/ MOORE P A.

PA (KYAW/) KYAW H.

PA (LAFLU/) LAFLEUR D W.  
 PA (SHTY/) SHI Y.  
 PA (JANAT/) JANAT F.  
 PA (ENDR/) ENDRESS G A.  
 PA (CART/) CARTER K C.  
 PA (BIRSE/) BIRSE C E.  
 XX  
 PI Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;  
 PI Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;  
 PI Endress GA, Carter KC, Birse CE;  
 XX  
 DR WPI; 2003-479549/45.

XX  
 PT New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease.  
 PT Disclosure; Page 9; 496pp; English.

XX  
 CC The invention describes a new isolated nucleic acid molecule comprising a sequence having at least 95% identity with a sequence comprising: (a) a polynucleotide (PN) fragment of a sequence comprising 420-345 bp, or its allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or (d) a PN that hybridizes under stringent conditions to any one of the sequences of (A)-(C). The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. This is the amino acid sequence of a novel human secreted protein fragment.

CC Sequence 20 AA;

Query Match 33.3%; Score 33; DB 6; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 5 LWNNTQDLEHS 18  
 Db 5 | ||||| : :  
 5 LVTNNQTQLQEAE 18

RESULT 13  
 ADG78515  
 ID ADG78515 standard; peptide; 20 AA.

AC AC  
 XX  
 DT 11-MAR-2004 (first entry)

XX  
 DE Human secreted protein #138.

KW Human; secreted protein; immune disorder; haematopoietic disorder; hyperproliferative disorder; infectious disease; inflammatory disorder; HIV; anaemia; thrombocytopenia; bleeding; stroke; myocardial infarction; Addison's disease; rheumatoid arthritis; dermatitis; Grave's disease; multiple sclerosis; glomerulonephritis; diabetes; graft-versus-host disease; inflammatory bowel disease; cancer; bacterial infection; viral infection; parasitic infection; osteoporosis; Alzheimer's disease; Parkinson's disease or ulcers. The sequences may also be used as food additives or preservatives, or for modulating mammalian mental or physical characteristics. The nucleic acids are also used in chromosome mapping, in forensic biology or as molecular weight markers. This sequence represents a human secreted protein of the invention.

XX  
 SQ Sequence 20 AA;

Query Match 33.3%; Score 33; DB 8; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 5 LWNNTQDLEHS 18  
 Db 5 | ||||| : :  
 5 LVTNNQTQLQEAE 18

RESULT 14  
 ADN60818  
 ID ADN60818 standard; peptide; 20 AA.  
 XX  
 AC ADN60818;  
 XX  
 DT 01-JUL-2004 (first entry)

XX  
 DE Human secreted polypeptide #149.

XX  
 KW Human; secreted polypeptide; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast; liver; cardiovascular disorder; cerebral ischaemia; nervous system disorder; Alzheimer's disease;

XX  
 PD 13-NOV-2003.  
 XX  
 PF 28-MAR-2001; 2001US-00818683.  
 XX  
 PR 05-MAY-1999; 99US-00305736.



XX  
DE FIV principal immunodominant domain in a HIV-1 context.  
XX  
KW Feline immunodeficiency virus; principal immunodominant domain; mutant;  
KW lentivirus; envelope protein; neutralising antibody; vaccine.  
XX  
OS Feline immunodeficiency virus i.  
OS Human immunodeficiency virus i.  
XX  
PA Chimeric.  
XX  
PN WO9630527-A1.  
XX  
PD 03-OCT-1996.  
XX  
PF 26-MAR-1996; 96WO-FR000449.  
XX  
PR 27-MAR-1995; 95FR-00003566.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Pancino G, Sonigo P;  
XX  
DR WPI; 1996-455372/45.  
XX  
PT Mutant lenti-virus Env Protein principal immuno-dominant domains - can  
PT produce neutralising antibodies to protect against e.g. FIV or HIV, but  
PT do not produce facilitating antibodies.  
XX  
PS Claim 3; Page 19; 38pp; French.  
XX  
CC The present sequence is a specifically claimed example of a novel peptide  
CC fragment which is a mutant of the wild-type (w.t.) principal  
CC immunodominant domain (PID) of human immunodeficiency virus such that an  
CC Env protein containing the fragment retains the ability to produce  
CC neutralising antibodies (Abs) but does not produce facilitating or  
CC deleterious Abs against the w.t. PID. The mutated Env protein can be used  
CC for producing vaccines against HIV. In addition to vaccination, the  
CC peptide fragment is useful as a diagnostic reagent, specifically to  
CC distinguish between Abs produced in response to vaccination and those  
CC resulting from viral infection. Also, the results of anti-HIV vaccination  
CC can be monitored using the peptide. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 18 AA;  
Query Match 32.3%; Score 32; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 7e+02; Mismatches 5; Conservative 1; Indels 4; Gaps 0; Gaps 0;  
Matches 5; Mismatches 4; Indels 0; Gaps 0;  
QY 5 IWMNQTLF 14  
ID :||| | |  
Db 1 IWGCQNQNPFF 10  
XX  
RESULT 17  
AAW07984  
ID AAW07984 standard; Peptide; 19 AA.  
XX  
AC AAW07984;  
XX  
DT 16-OCT-2003 (revised)  
DT 03-FEB-1997 (first entry)  
XX  
DB gp41 peptide MN-13.  
XX  
KW HIV; gp41; HIV-IIIB strain; HIV-1 transmission; foetal transmission;  
KW neutralising antibody; passive immunisation; anti-idiotypic antibody;  
KW gp41; vaccine; active immunotherapy.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN US5556744-A.

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XX  
PD 17-SEP-1996.  
XX  
PF 24-MAR-1994; 94US-00218025.  
XX  
PR 29-MAY-1992; 92US-00891451.  
XX  
PA (UPF-) UNIV PENNSYLVANIA.  
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
XX  
PI Williams WV, Weiner DB, Ugen KE;  
XX  
DR WPI; 1996-422980143.  
XX  
PT Determining the likelihood of maternal transmission of HIV-1 to foetus -  
PT by measuring maternal reactivity with specific gp120 and gp41 derived  
PT peptide(s), also used for diagnosing HIV in infants.  
XX  
PS Example 7; Col 101-102; 63pp; English.  
XX  
AAW07980-W07987 represent HIV gp41 peptides that can be used in the  
CC method of the invention. The method of the invention is for determining  
CC whether or not a mother will transmit HIV-1 to a foetus. The method  
CC comprises incubating a sample from the HIV-infected mother, with a  
CC collection of HIV peptides. The HIV peptides includes at least one of  
CC these sequences, and at least one HIV gp120 derived peptide (see AAW07909  
CC -W07917). The number of peptides that react with the sample is  
CC determined, and this number is compared with a standard that shows  
CC pattern reactivity for a patient of transmission status. A non-  
CC transmissible HIV sample is indicated if the test sample reacts with twice  
CC as many peptides as the standard. The method detects the presence of  
CC neutralising antibodies that protect against mother to infant  
CC transmission of HIV. These sequences can also be used in vaccines to  
CC protect against transmission. Antibodies against these sequences can be  
CC used for passive immunisation, and to generate anti-idiotypic antibodies  
CC for use in vaccines or active immunotherapy. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 19 AA;  
Query Match 32.3%; Score 32; DB 2; Length 19;  
Best Local Similarity 62.5%; Pred. No. 7.4e+02; Mismatches 5; Conservative 1; Indels 2; Gaps 0; Gaps 0;  
Matches 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SSDGIMNN 8  
ID :||| | |  
Db 1 SLDIWN 8  
XX  
RESULT 18  
AAGG64600  
ID AAGG64600 standard; peptide; 15 AA.  
XX  
AC AAGG64600;  
XX  
DT 31-OCT-2001 (first entry)  
XX  
DE Human excitatory amino acids transporter 17 peptide.  
XX  
KW Human; excitatory amino acid transporter 17; cytostatic; virucidal;  
KW immunodulatory; antiinflammatory; haemostatic; malignant tumour; HIV;  
KW human immunodeficiency virus; infection; immunological disease;  
KW substance metabolic disorder; neural mental illness;  
KW embryonic development disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200166726-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-CN000172.

PR 10-MAR-2000; 2000CN-00111957.  
 XX  
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX  
 PI Mao Y, Xie Y;  
 XX DR WPI; 2001-557864/62.  
 CC Human excitatory amino-acid transporter 17 and encoded polynucleotide, an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-4, IL-12, IL-18 or gamma-interferon. The cells are human cells and contain a nucleic acid encoding a mutant HSV protein or a nucleic acid encoding the polypeptide sufficient for virus-like particle assembly but devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
 CC The genome is devoid of late domain motifs capable of effecting viral budding. The composition also comprises a compound capable of interfering with the protein-protein interaction between a host cell protein capable of binding a late domain motif and a HSV protein containing a late domain motif. The composition further comprises another HSV protein or its immunogenic fragment, and/or a nucleic acid encoding the other HSV protein or the immunogenic fragment. The present sequence is a mutant HSV peptide, derived from the wild-type peptide ADU38601, used to illustrate the invention.  
 CC  
 CC development disorder and growth and development disturbance illness. The present sequence is that of a human excitatory amino-acid transporter 17 peptide.  
 CC  
 SQ Sequence 15 AA:  
 Query Match 31.3%; Score 31; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SDGLW 6  
 Db 8 SDGLW 12  
 RESULT 19  
 ADU38603  
 ID ADU38603 standard; peptide; 15 AA.  
 XX  
 AC ADU38603;  
 XX DT 06-MAY-2004 (first entry)  
 XX HSV-4 BFLF2 protein late domain motif mutant peptide #2.  
 XX Virucide; HSV infection; antiviral; late domain motif; muten; mutant.  
 XX OS Human herpesvirus 4.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 6 /note= "Wild-type residue replaced with Arg"  
 FT  
 PN WO200400927-A2.  
 XX PD 29-JAN-2004.  
 XX PF 21-JUL-2003; 2003WO-US022828.  
 PR 19-JUL-2002; 2002US-0397265P.  
 PR 19-JUL-2002; 2002US-0397477P.  
 PR 03-MAR-2003; 2003US-0451903P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX PI Buschle M, Rabel A, Klade C, Mattnier F, Otava O, Vytytska O;  
 PI Zauner W, Zinke S, Kirlappos H;  
 XX DR WPI; 2004-269899/25.  
 XX  
 PR Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.  
 XX PS Example 1; Page 30; 73pp; English.  
 XX CC The invention relates to a novel method for isolating Hepatitis C virus (HCV) peptides (Hps). The method of the invention has virucide activity,  
 CC

CC and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the cells, a T cell clone or a T cell population or preparation is useful for identifying heteroclitic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match Best Local Similarity 31.3%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 2 NTNGSWHINNTAL 14

RESULT 21

ID ADL25931 standard; peptide; 15 AA.

AC ADL25931;

XX DT 17-JUN-2004 (first entry)

DB Synthetic peptide A118 derived from a conserved region of HCV.

XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

XX OS Synthetic.

XX PN WO2004024182-A2.

XX PD 25-MAR-2004.

XX PP 27-AUG-2003; 2003WO-EP009482.

XX PR 13-SEP-2002; 2002AT-00001376.

XX PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Habel A, Klade C, Mattnier F, Otava O, Vyrvyska O; PI Zauner W, Zinke S, Kirlappos H;

XX DR WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Example 1; Page 30; 73pp; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Example 1; Page 30; 73pp; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Sequence 15 AA;

Query Match Best Local Similarity 38.5%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 3 NTNGSWHINNTAL 15

RESULT 22

ID ADL25933 standard; peptide; 15 AA.

AC ADL25933;

XX DT 17-JUN-2004 (first entry)

DB Synthetic peptide A120 derived from a conserved region of HCV.

XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA; major histocompatibility complex; human leukocyte antigen.

XX OS Synthetic.

XX PN WO2004024182-A2.

XX PD 25-MAR-2004.

XX PP 27-AUG-2003; 2003WO-EP009482.

XX PR 13-SEP-2002; 2002AT-00001376.

PR 27-FEB-2003; 2003WO-EP002005.

PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Habel A, Klade C, Mattnier F, Otava O, Vyrvyska O; PI Zauner W, Zinke S, Kirlappos H;

XX DR WPI; 2004-269899/25.

PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Example 1; Page 30; 73pp; English.

XX CC The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has virucide activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the PT molecule by separating the complex from the HCV-peptides which do not bind to the molecule.

XX PS Sequence 15 AA;

Query Match Best Local Similarity 38.5%; Score 31; DB 8; Length 15; Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNWNTQL 13  
Db 1 NTNGSWHINNTAL 13

RESULT 23

ID ADL25932 standard; peptide; 15 AA.

Query Match

31.3%; Score 31; DB 8; Length 15;



XX New hepatitis C virus (HCV) peptides and mosaic antigen composition  
 PT comprising the peptides, useful as immunoreagents for detecting HCV  
 PT antibodies infection, or as an immunogen for stimulating production of  
 PT antibodies against HCV.  
 XX Example 4; Page 33; 5pp; English.

CC The present sequence is that of peptide MDL-16 comprising amino acid  
 CC residues 412-429 of the hepatitis C virus (HCV) polyprotein E2 region. A  
 CC panel of HCV polyprotein-derived peptides was tested for immunoreactivity  
 CC with a commercially available human serum panel. All of the  
 CC immunoreactivity was concentrated within the core region between amino  
 CC acids 1 to 80. MDL-16 exhibited low and inconsistent immunogenicity. The  
 CC invention provides a highly immunoreactive mosaic antigen composition  
 CC (MAC) comprising 2 or more HCV immunoreactive peptides (see AAM5081-27),  
 CC each of which is immobilized to a carrier. The unique combination of HCV  
 CC core peptides in the MAC provides higher specificity and sensitivity for  
 CC detection of human antibodies specificity to HCV in rapid HCV diagnostic  
 CC applications. An in vitro diagnostic method for detecting anti-HCV  
 CC antibodies in a test sample and a diagnostic test kit are provided which  
 CC use the MAC as an immunoreagent. The HCV MAC may also potentially be used  
 CC as an immunogen in vaccine compositions. (Updated on 07-AUG-2003 to  
 XX correct OS file.)

SQ Sequence 17 AA;

Query Match	31.3%	Score	31;	DB	5;	Length	17;
Best Local Similarity	38.5%	Pred	No.	9.3e-02;		Gaps	0;
Matches	5;	Mismatches	3;	Indels	0;		
Qy	1 SSDGLWNMNOTQL 13	Db	4 NTNGSWHINRHTAL 16				

RESULT 26

ID	ABW01700	AC	AD059249;
ID	ABW01700 standard; protein; 19 AA.	XX	
XX		DT	15-JUL-2004 (first entry)
AC	ABW01700;	XX	Toxoplasma gondii TATI-3 activating domain peptide.
XX		DE	
DT	12-FEB-2004 (first entry)	XX	gene activation; tetracycline-controlled transactivator;
XX	Toxoplasma gondii TATI-1 transacting factor activation domain.	KW	tetracycline repressor; TeR; TATI-1; TATI-3; vaccine;
XX	Cellular vaccine; tetracycline repressor; TetR; transacting factor;	KW	parasite infection; protozoacide.
XX	protozoal infection; gene therapy; TATI.	OS	Toxoplasma gondii.
OS	Toxoplasma gondii.	XX	GB2388112-A.
XX		PN	
XX	US2003185851-A1.	XX	05-NOV-2003.
PP	20-MAR-2002; 2002US-00102143.	PD	
PR	20-OCT-2003.	PF	20-MAR-2002; 2002GB-00006595.
XX		PR	20-MAR-2002; 2002GB-00006595.
PN		PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX		PI	Soldati D, Meissner M;
XX		XX	WPI; 2003-880573/82.
PP		DR	N-55DB; AD059248.
PR		XX	
XX		PT	New nucleic acid construct comprising tetracycline repressor operatively PT linked to a transacting factor of Toxoplasma gondii, useful in producing PT vaccines to treat or prevent infections caused by Apicomplexan parasites.
PS		XX	
PS		PT	This invention relates to a novel control system for regulating gene PT activation in Toxoplasma gondii ( <i>T. gondii</i> ) using tetracycline-controlled PT transactivators. Specifically, it refers to a nucleic acid construct PT comprising the tetracycline repressor (TeR) operatively linked to a <i>T.</i> PT <i>gondii</i> transacting factor (TATI-1 or TATI-3) and an activating domain.
XX		CC	The present invention describes this construct as useful for preparing a CC vaccine for the treatment or prophylaxis of an infection caused by a CC protozoan parasite selected from, for example, <i>T. gondii</i> , <i>Plasmodium</i> CC <i>falciparum</i> , <i>Trypanosoma brucei</i> , <i>Entamoeba histolytica</i> or <i>Giardia lamblia</i> .
XX		CC	Furthermore, it can be used to create attenuated strains of the parasites
PT		CC	that can act as vaccines to protect against Apicomplexan parasite
PT		CC	infection, and also identify essential genes that could provide novel
XX		CC	drug targets. As such, these compositions can be referred to as
PS		CC	protozoacides. This peptide sequence is the <i>T. gondii</i> TATI-3 activating
XX		CC	domain peptide, given in an exemplification of the invention.

The present invention relates to nucleic acid and cellular vaccines which

XX SQ Sequence 19 AA;  
 XX Query Match 31.3%; Score 31; DB 7; Length 19;  
 XX Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 XX Matches 4; Conservative 2; Mismatches 0; Indels 0;  
 XX Gaps 0;  
 Qy 6 WNNNOTQFLU 15  
 Db 8 WNNTQPYLGL 17

RESULT 28  
 ADR26471  
 ID ADR26471 standard; peptide; 20 AA.  
 XX  
 AC ADR26471;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Isomaltose manufacture method enzyme-derived peptide #19.  
 XX DE isomaltose; alpha-isomaltosyl gluco-sugar synthase; alpha-1; 4-glucosyl bond; isomaltitol;  
 KW alpha-isomaltosyl glucosugar; alpha-1; 6-glucosyl bond; isomaltitol;  
 KW health food; beverage; fodder; cosmetic; pharmaceutical; humectant;  
 KW osmotic pressure regulators; sugar crystallization inhibitor;  
 KW starch aging inhibitor.  
 OS Sporosarcina globispora.  
 XX WO2003033717-A1.  
 XX PN PD 24-APR-2003.  
 XX PF 18-OCT-2002; 2002WO-JP010845.  
 XX PR 18-OCT-2001; 2001JP-00321182.  
 XX PR 30-AUG-2002; 2002JP-00252609.  
 XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX PI Kubota M, Nishimoto T, Sonoda T, Fukuda S, Miyake T;  
 DR XX WPI; 2003-430348/40.  
 XX PT Manufacture of isomaltose in two-step process from specified sugar types  
 PT using specified enzymes, for manufacture of isomaltitol and use in  
 foodstuffs, fodder, pharmaceuticals and cosmetics.  
 XX PS Disclosure; Page 205; 260pp; Japanese.  
 XX  
 CC The invention relates to the manufacture of isomaltose by making one or  
 more alpha-isomaltosyl gluco-sugar synthase from *Bacillus globisporus* N75  
 (FERM BP-7591), *Arthrobacter globiformis* Al9 (FERM BP-7590) and  
*Arthrobacter ramous* Sl (FERM BP-7592), in the presence or absence of  
 alpha-1-isomaltosyl transferase from *Bacillus globisporus* N75 (FERM BP-  
 7591) and/or *Arthrobacter globiformis* Al9 (FERM BP-7590) act on a sugar  
 of glucose polymerization degree of two or more having alpha-1,4-glucosyl  
 bonds as the bonding of the non-reducing terminal to give a alpha-  
 isomaltosylglucosugar with glucose polymerization degree of three or more  
 having a alpha-1,6-glucosyl bond as a non-reducing terminal and alpha-1,4  
 -glucosyl bonds as the other terminals and/or cyclol-[6]-alpha-D-  
 glucopyranosyl-(1->)alpha-D-glucopyranosyl-(1->)alpha-D-glucopyranosyl-  
 (1->)alpha-D-glucopyranosyl-(1->), acting on this with isomaltose release  
 enzyme and collecting the isomaltose. The isomaltose and isomaltitol are  
 used in health foods and beverages, fodder and feeds, cosmetics and  
 pharmaceuticals, and luxury articles, as humectant, osmotic pressure  
 regulators, low sweeteners, sugar crystallization inhibitors, and starch  
 aging inhibitors. This sequence represents a peptide derived from one of  
 the above proteins.

XX Sequence 20 AA;  
 XX  
 XX Query Match 31.3%; Score 31; DB 7; Length 20;  
 XX Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
 XX Matches 4; Conservative 2; Mismatches 0; Indels 0;  
 XX Gaps 0;  
 Qy 3 DGLMN 8  
 Db 4 DGWHN 9

RESULT 29  
 ADH80940  
 ID ADH80940 standard; peptide; 20 AA.  
 XX  
 AC ADH80940;  
 XX DT 15-APR-2004 (first entry)  
 XX DE HIV hypervariable epitope construct (HEV) #5.  
 XX DE antimicrobial; vaccine; immunogenic peptide mixture; immunogenic epitope;  
 KW pathogen; reactive immunity; human immunodeficiency virus; HIV;  
 KW hypervariable epitope construct.  
 XX OS Human immunodeficiency virus 1.  
 XX KEY Location/Qualifiers  
 FT Misc-difference 11 /note= "Thr, Ser"  
 FT Misc-difference 13 /note= "Ile, Thr"  
 FT  
 XX PN US2002183484-A1.  
 XX PD 05-DEC-2002.  
 XX PF 08-FEB-2002; 2002US-00072084.  
 XX PR 09-OCT-1998; 98US-0103642P.  
 PR 08-OCT-1999; 99US-00414484.  
 XX PA (TORR) TORRES J V.  
 XX PI Torres JV;  
 XX DR WPI; 2003-328635/31.  
 XX PT Preparation of immunogenic peptide mixtures for e.g. producing vaccines,  
 PT by obtaining immunogenic epitope sequences having common residue regions  
 PT and variable residues, and determining frequency of amino acids at the  
 PT variable residues.  
 XX PS Example 1; FIG 3; 30pp; English.  
 XX CC The invention describes the preparation of an immunogenic peptide  
 mixture. The mixture is prepared by obtaining immunogenic epitope  
 sequences of a pathogen having a common residue region and at least one  
 variable residue, determining the frequency with which different amino  
 acids are found at the variable residue and synthesising a peptide.  
 CC mixture comprising up to 100 different peptides using the amino acids.  
 CC the peptide mixture is useful in the production of vaccines, therapeutic  
 agents and diagnostic kits against pathogenic organisms, e.g. viruses and  
 CC parasites. The inventive method produces less complex immunogenic peptide  
 formulation than those described in the prior art, while retaining  
 CC optimum immunogenicity. The resulting immunogenic peptide mixture evokes  
 CC broadly reactive immunity. This is the amino acid sequence  
 CC immunodeficiency virus type 1 hypervariable epitope construct used in the  
 CC immunogenic peptide mixture of the invention.  
 XX Sequence 20 AA;

Query Match 31.3%; Score 31; DB 7; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;



Query Match 31.3%; Score 31; DB 8; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	7	NNNQTOFLIE	16
Db	6	NYNQNQLIME	15

RESULT 32

ADE8906 standard; peptide; 10 AA.

XX ADE8906;

XX DT 29-JAN-2004 (first entry)

XX Interleukin 13 receptor subunit alpha 2 immunogenic peptide.

XX immune response; interleukin 13 receptor subunit alpha 2; IL-13Ralpha2;

XX anti-cancer; vaccine; human; immunogenic.

XX Synthetic.

OS Homo Sapiens.

XX WO2003092717-A1.

XX PD 13-NOV-2003.

XX PP 22-MAR-2002; 2002WO-US008983.

XX PR 22-MAR-2002; 2002WO-US008983.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Debinski W, Christensen N, Mintz A;

XX DR WPI; 2003-903570/82.

XX PT Stimulating an immune response against IL-13Ralpha2 in a subject having

PT or at risk for developing a disease, e.g. cancer, by formulating an anti-

PT cancer vaccine comprising an agent that can stimulate the immune response

PT against.

PS Example 3; Page 43; 67pp; English.

XX The present invention describes a method for stimulating an immune

CC response against Interleukin 13 receptor subunit alpha 2 (IL-13alpha2)

CC in a subject having or at risk for developing a disease having cells

CC expressing IL-13Ralpha2. The method comprises formulating an anti-cancer

CC vaccine comprising an agent that can stimulate an immune response against

CC IL-13Ralpha2 when administered to an animal, outside of the subject; and

CC administering the vaccine to the subject to stimulate an immune response

CC against IL-13Ralpha2 in the subject. Also described: (1) a composition

CC for stimulating the immune response against IL-13Ralpha2 when

CC administered to an animal, comprising an isolated gene that can stimulate

CC an immune response against IL-13Ralpha2 when administered to the animal,

CC and carrier; (2) a method for directing an antibody to cells expressing

CC IL-13Ralpha2 in a subject, by formulating a pharmaceutical composition

CC outside of a subject, where the composition comprises an antibody that

CC specifically binds IL-13Ralpha2 and a carrier; and administering the

CC pharmaceutical composition to the subject to allow the antibody to

CC specifically bind to the cells expressing IL-13Ralpha2 in the subject;

CC and (3) a pharmaceutical composition comprising the antibody that

CC specifically binds IL-13Ralpha2 and a carrier. The methods and

SQ composition are useful for stimulating an immune response against IL-

CC 13Ralpha2 in a subject having or at risk for developing a disease having

CC immunogenic peptide for IL-13Ralpha2. The present sequence represents an

CC the present invention.

RESULT 33

AAE10548 standard; peptide; 12 AA.

XX AAE10548;

XX DT 10-DEC-2001 (first entry)

XX DB Llama species antibody VH CDR3 #17.

XX Kappa antibody; camelid; anorectics; heavy chain variable domain; VH; HPL;

XX food; human gastric lipase; HGL; cosmetic control; body weight;

XX complementarity determining region 3; CDR3.

XX OS Lama sp.

XX PN EP1134231-A1.

XX PD 19-SEP-2001.

XX BP 20-FEB-2001; 2001EP-00200703.

XX PR 14-MAR-2000; 2000EP-00200930.

XX PA (UNIT ) UNILEVER NV.

XX RA (UNIT ) UNILEVER PLC.

XX DR Bezemer S, Van De Burg M, De Haard JMW, Tareilus E;

XX DR WPI; 2001-572718/65.

XX PT New antibody or its fragments for inhibiting human dietary enzymes,

PT useful for cosmetic control of body weight of human beings, comprises

PT heavy chain variable domain derived from immunoglobulin naturally devoid

PT of light chains.

XX PS Claim 4; Page 29; 37pp; English.

XX The patent discloses antibodies or their fragments comprising a heavy

CC chain variable domain (VHH) derived from an immunoglobulin naturally

CC devoid of light chain specific for inhibiting human dietary enzymes. The

CC antibodies of the invention are useful for the preparation of medicaments

CC or food for inhibiting the activity of one or more human dietary enzymes

CC especially human pancreatic lipase (HPL) or human gastric lipase (HGL)

CC which are useful for the cosmetic control of body weight of human beings.

CC The present peptide sequence is a complementarity determining region 3

CC (CDR3) of llama species (camelid) antibody VH region

XX SQ Sequence 12 AA;

Query Match 30.3%; Score 30; DB 4; Length 12;

Best Local Similarity 62.5%; Pred. No. 9.1e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLWN 8

Db 4 SYDGSWND 11

RESULT 34

ABB80837 standard; protein; 12 AA.

XX  
AC ABB80837;  
XX PR 12-AUG-1999; 99US-0148935P.  
XX DT 23-SEP-2002 (first entry)  
XX DE Heparin binding laminin alpha4 protein fragment.  
XX KW Laminin alpha4; heparin; signal transduction; transgenic; cancer;  
XX angiogenesis; cytostatic; vasotropic; gene therapy; mouse.  
OS Mus musculus.  
XX PN WO200248349-A1.  
XX PD 20-JUN-2002.  
XX PR 10-JUL-2001; 2001WO-JP005976.  
XX 12-DEC-2000; 2000JP-00376899.  
XX PA (KYOU ) KYOWA HAKKO KOGYO KK.  
XX PT Kitagawa Y, Shitara K, Ohki Y;  
XX DR WPI; 2002-490604/22.  
XX PT Polypeptides binding strongly to heparin for treatment of cancer and  
angiogenesis-related disorders.  
XX Example: Page 106; 129pp; Japanese.  
XX  
The invention relates to a polypeptide forming part of the laminin alpha4  
chain G domain, having molecular weight below 108 kDa, and capable of  
binding to heparin. The polypeptide can be used to inhibit heparin-  
binding signal transduction from cells. The polypeptide, encoding DNA,  
non-human transgenic animals and transgenic plants containing the  
recombinant DNA can all be used for the treatment and prevention of  
cancer and angiogenesis-related diseases. The present sequence represents  
a fragment of the heparin binding mouse laminin alpha4 protein  
XX Sequence 12 AA;

Query Match	30.3%;	Score 30;	DB 5;	Length 12;
Best local Similarity	57.1%;	Pred. No.	9.1e+02;	
Matches	4;	Conservative	3;	Mismatches 0;
		Indels	0;	Gaps 0;

Oy 2 SDGLWNN 8  
Db 6 NDGLWHD 12

RESULT 35

ID AAB73315 standard; peptide; 14 AA.

XX  
AC AAB73315;  
XX DT 22-MAY-2001 (first entry)  
XX  
DE Human PC-LECTIN extracellular domain peptide, SEQ ID NO:25.  
XX KW Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis;  
KW larvin homologue; Prostate cancer antigen; overexpression;  
KW androgen-dependent prostate cancer; diagnosis; prognosis;  
KW extracellular domain; antigenic; antibody.  
Homo sapiens.  
XX OS Homo sapiens.  
XX PN WO00112811-A1.  
XX PD 22-FEB-2001.  
XX PN 11-AUG-2000; 2000WO-US022065.

XX  
AC ABB80837;  
XX PR 12-AUG-1999; 99US-0148935P.  
XX DE (UROG-) UROGENESYS INC.  
XX PI Afar DEH, Hubert RS, Jakobovits A, Raitano AB;  
XX DR WPI; 2001-211222/21.  
XX PT New PC-LECTIN polynucleotide encoding a transmembrane antigen over  
expressed in human prostate cancer, useful for the prognosis, diagnosis  
and treatment of prostate cancer.  
XX PS Claim 4; Page 79; 116pp; English.  
XX  
The invention relates to a novel human C-type lectin transmembrane  
antigen, PC-LECTIN (AAB73319) and cDNA encoding it (AAP7004). The  
expression of the human PC-LECTIN gene is normally restricted to the  
testis, but is highly overexpressed in prostate cancer. PC-LECTIN  
expression is higher in androgen-dependent prostate tumors compared with  
androgen-independent prostate tumors, and expression is therefore likely  
to be dependent on the presence of androgen. Human PC-LECTIN therefore  
represents a diagnostic and therapeutic target for prostate cancer.  
Particularly androgen-dependent prostate cancer. Human PC-LECTIN exhibits  
homology to hamster laylin (44.9% identity over a 265 residue overlap),  
but is not thought to be the human orthologue of laylin, as diverges  
significantly in a key functional domain proposed for the laylin  
protein. Human PC-LECTIN or an immunogenic portion thereof, a vector  
encoding PC-LECTIN, a PC-LECTIN antisense nucleotide, a PC-LECTIN  
nucleotide-targetted ribozyme, or an anti- PC-LECTIN antibody may be used  
CC to prepare a composition for treating a patient with a cancer,  
CC particularly prostate cancer, but also breast, bladder, lung, bone,  
CC colon, pancreatic, testicular, cervical or ovarian cancers that express  
CC PC-LECTIN. PC-LECTIN proteins are also useful for diagnosing the presence  
CC of cancer. PC-LECTIN antibodies and nucleotides are useful in the  
CC treatment (e.g., antisense therapy), diagnosis and/or prognosis of  
CC prostate cancer and other PC-LECTIN-expressing cancers. PC-LECTIN  
CC antibodies may also be used as drug targeting agents. The PC-LECTIN  
CC nucleotides and proteins may additionally be used in drug discovery to  
CC identify molecules that modulate PC-LECTIN function or expression. The  
CC present sequence represents a human PC-LECTIN extracellular domain  
CC peptide used to raise anti-PC-Lectin antibodies  
XX Sequence 14 AA;

Query Match	30.3%;	Score 30;	DB 4;	Length 14;
Best local Similarity	55.6%;	Pred. No.	1.1e+03;	
Matches	5;	Conservative	0;	Mismatches 4;
		Indels	0;	Gaps 0;

Oy 4 GLWNNNQDQ 12  
Db 1 GLWRNGDQ 9

RESULT 36

ID ABJ00795  
AC ABJ00795 standard; peptide; 14 AA.  
XX DT 05-SEP-2002 (first entry)  
XX DE ABJ00795 lymphocyte affinity maturation library peptide #69.  
XX KW B lymphocyte stimulator protein binding protein; BLyS; immune disease;  
KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;  
KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
KW immunosuppressive; nephrotoxic; anti-rheumatic; antiarthritic;  
KW neuroprotective; cytosolic; immunomodulant; antitumour; anti-HIV;  
KW antiasthmatic; antiallergic; immunosimulant; antihaemolytic;  
KW dermatological; antiinflammatory; cardiotonic; ophthalmological; uropathic;  
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

XX  
 OS Unidentified.  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PT New B-Lymphocyte stimulator binding polypeptide comprises a specified amino acid sequence.  
 XX  
 PT isolating Blys or Blys-like polypeptide from an invention.  
 XX  
 PT sequence.  
 XX  
 PS Claim 6; Page 89; 269pp; English.  
 XX  
 CC The invention relates to a B Lymphocyte Stimulator (Blys) binding polypeptide. Blys binding peptides bind Blys or Blys-like proteins reversibly or irreversibly. The binding peptides are used in detection, isolation and/or purification of Blys in a solution such as water or a buffer solution, as well as any fluid and/or cell obtained from an individual biological fluid, body tissue, body cell, cell line, tissue culture or other source containing Blys or Blys-like polypeptides. The biological fluids include sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and mucus. Sequences ABG33406-33415, ABG33423-3355, ABG33588-33846, ABG33848-33850 and ABG33852-33862 represent Blys binding peptides of the invention  
 XX  
 SQ Sequence 14 AA;  
 CC  
 CC Lymphocyte stimulator (Blys), Blys receptor expression or activity; cells of haematopoietic origin, or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production; B cell proliferation and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide  
 CC  
 XX  
 SQ Sequence 14 AA;  
 CC  
 CC Query Match 30.3%; Score 30; DB 5; Length 14;  
 CC Best Local Similarity 38.5%; Pred. No. 1.1e+03;  
 CC Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 CC  
 OY 5 LWNNTQFLLEH 17  
 OY :|:||:||:  
 OY 2 IWDPLTKMLPH 14  
 OY :|:||:||:  
 OY 5 LWNNTQFLLEH 17  
 OY :|:||:||:  
 OY Db 2 IWDPLTKMLPH 14  
 OY :|:||:||:  
 OY Result 38  
 ID ARB5392  
 ID ARB5392 standard; peptide; 15 AA.  
 XX  
 AC AAR85392;  
 XX  
 DT 13-JUN-1996 (first entry)  
 XX  
 DE HTLV-IIIB envelope glycoprotein antigenic peptide, SP-15.  
 XX  
 KW Human immunodeficiency virus; HIV; HTLV-IIIB; envelope; glycoprotein; KW hydrophobic; immunisation; antibody production; fusion peptide; SP-1; KW conjugate; carrier.  
 XX  
 OS Synthetic.  
 XX  
 PN W09529700-A1.  
 XX  
 PD 09-NOV-1995.  
 XX  
 PR 28-APR-1995; 95WO-US005465.  
 XX  
 PR 29-APR-1994; 94US-00235305.  
 XX  
 PA (UVDU-) UNIV DUKE.  
 XX  
 PI Haynes BF, Parker TJ;  
 XX  
 WPI; 1995-392926/50.  
 XX  
 PT New peptide(s) corresponding to HIV sequences - used for inducing protective immunity to HIV and in the treatment of e.g. auto-immune disease, infectious disease or tumours.  
 XX  
 PS Example 1; Page 42; 128pp; English.  
 XX  
 CC AAR5388-R8593 synthetic peptides with hydrophilic amino acid sequences of the HIV isolate HTLV-IIIB envelope protein. These peptides can be covalently linked to a carrier molecule. The conjugate produced is capable of inducing the production of high titres of protective, type-  
 CC

CC specific; anti-HIV antibodies. Helper T cells and cytotoxic T cells are  
 CC also activated by the peptide immunogens  
 XX  
 SQ Sequence 15 AA;

Query Match	30.3%; Score 30; DB 2; Length 15;
Best Local Similarity	41.7%; Pred. No. 1.2e+03;
Matches	5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGLMWNNQTOOLF 14  
 Db 4 DGGMNSNNESIIP 15

RESULT 39

AAW19031	PN
ID AAW19031	AAW19031; Standard; peptide; 15 AA.
XX	XX
AC AAW19031;	XX
XX	XX
DT 16-JAN-1998 (first entry)	XX
XX	XX
SP-15 region of HIV envelope glycoprotein.	XX
DE	XX
XX	XX
KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;	XX
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;	XX
KW immune response; infection; neutralisation; SP-15 region.	XX
OS Human immunodeficiency virus.	XX
OS	XX
PN WO9714436-A1.	XX
XX	XX
PD 24-APR-1997.	XX
XX	XX
PP 18-OCT-1996; 96WO-US016911.	XX
XX	XX
PR 20-OCT-1995; 95US-00546515.	XX
PR 09-FEB-1996; 96US-00599266.	XX
PA (UYDU-) UNIV DUKE.	XX
PI Haymes BF, Parker TJ;	XX
DR WO9714436-A1.	XX
XX	XX
PR 09-FEB-1996; 96US-00599266.	XX
PA (UYDU-) UNIV DUKE.	XX
XX	XX
PR 20-OCT-1995; 95US-00546515.	XX
PR 09-FEB-1996; 96US-00599266.	XX
PT (UYDU-) UNIV DUKE.	XX
PI Haymes BF, Parker TJ;	XX
DR WO9714436-A1.	XX
XX	XX
PR Synthetic human immunodeficiency virus vaccine - comprising hydrophilic peptide corresponding to at least 1 antigenic determinant of envelope glyco-protein recognised by B lymphocytes.	XX
PT	XX
PT peptide corresponding to at least 1 antigenic determinant of envelope glyco:protein recognised by B lymphocytes.	XX
PS Example 1; Page 37; 104pp; English.	XX
PS	XX
XX	XX
CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic determinant of human immunodeficiency virus (HIV) envelope (env) glycoprotein (gp) recognised by B lymphocytes, i.e. the present sequence, when covalently linked to a carrier molecule, induces the production of high titer of protective, type specific anti-HIV antibodies (Ab) in a mammal. The peptide can be used in vaccines for producing a protective immune response to HIV infection, while a HIV neutralising Ab can be induced in a primate by administering a composition comprising HIV envelope peptides that disrupt gp120/gp41 interactions	XX
SQ Sequence 15 AA;	XX

Query Match 30.3%; Score 30; DB 2; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGLMWNNQTOOLF 14  
 Db 4 DGGMNSNNESIIP 15

ADL25934  
 ID ADL25934 Standard; peptide; 15 AA.  
 XX  
 AC ADL25934;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Synthetic peptide A121 derived from a conserved region of HCV.  
 XX  
 KW HCV; hepatitis C virus; viaccine; vaccine; MHC; HLA;  
 KW major histocompatibility complex; human Leukocyte antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200424182-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PR 27-AUG-2003; 2003WO-EP00942.  
 XX  
 PR 13-SEP-2002; 2002AT-00001376.  
 PR 27-FEB-2003; 2003WO-EP002055.  
 PR 11-JUL-2003; 2003EP-00450171.  
 XX  
 PA (INVE-) INTERCELL AG.  
 XX  
 PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vyryvtska O;  
 PI Zauner W, Zinke S, Kirlappos H;  
 XX  
 DR WO2004-249899/25.  
 XX  
 PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the molecule by separating the complex from the HCV-peptides which do not bind to the molecule.  
 XX  
 PS Example 1; Page 30; 73pp; English.  
 The invention relates to a novel method for isolating Hepatitis C Virus (HCV) peptides (Hps). The method of the invention has viaccine activity, and may be useful in producing a vaccine. The method is useful for isolating Hepatitis C Virus peptides (Hps) which have a binding capacity to a MHC/HLA molecule or a complex comprising the HCV-peptide and the MHC/HLA molecule for preparing a vaccine against HCV infection. The T cells, a T cell clone or a T cell population or preparation is useful for identifying heterocyclic epitopes or for preparing a composition for treating HCV infection. The present sequence represents a synthetic peptide derived from a conserved region of HCV.  
 XX  
 SQ Sequence 15 AA;

Query Match	30.3%; Score 30; DB 8; Length 15;
Best Local Similarity	41.7%; Pred. No. 1.2e+03;
Matches	5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SDGLMWNNQTOOLF 13  
 Db 1 TNGSWHINTL 12

Search completed: December 30, 2004, 16:28:14  
 Job time : 160 secs

OM protein - protein search, using sw model  
Run on: December 30, 2004, 16:04:21 ; Search time 38 Seconds  
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30	31	42	42	42.4	42.4	269	2	H91091
31	32	42	42	42.4	42.4	269	2	C85937
32	33	42	42	42.4	42.4	278	2	S73153
33	34	42	42	42.4	42.4	326	1	VGXK37
34	35	42	42	42.4	42.4	400	2	A97544
35	36	42	42	42.4	42.4	400	2	AC2754
36	37	42	42	42.4	42.4	457	2	T05439
37	38	42	42	42.4	42.4	620	2	AL58932
38	39	42	42	42.4	42.4	1014	2	S75724
39	40	42	42	42.4	42.4	1161	2	D872645
40	41	42	42	42.4	42.4	1161	2	T03076
41	42	41.5	41.9	41.9	41.9	786	2	T39034
42	43	41.5	41.9	41.9	41.9	1254	1	JQ1101
43	44	41.5	41.9	41.9	41.9	1254	1	T07363
44	45	41.5	41.9	41.9	41.9	326	1	VGXK25
45	46	41.5	41.9	41.9	41.9	326	1	VGXK35
46	47	41.5	41.9	41.9	41.9	326	1	VGXKRN
47	48	41.5	41.9	41.9	41.9	326	1	VGXKRN
48	49	41.5	41.9	41.9	41.9	326	1	VGXKRN
49	50	41.5	41.9	41.9	41.9	486	1	A48925
50	51	41.5	41.9	41.9	41.9	494	2	AC2424
51	52	41.5	41.9	41.9	41.9	569	2	P86646
52	53	41.5	41.9	41.9	41.9	656	2	C86934
53	54	41.5	41.9	41.9	41.9	656	2	ET57465
54	55	41.5	41.9	41.9	41.9	955	2	A60990
55	56	41.5	41.9	41.9	41.9	1455	1	A48925
56	57	41.5	41.9	41.9	41.9	1464	1	JQ1101
57	58	40.5	40.9	40.9	40.9	226	2	T27843
58	59	40.5	40.9	40.9	40.9	720	2	B75540
59	60	40.5	40.9	40.9	40.9	228	2	AC2297
60	61	40.5	40.9	40.9	40.9	260	1	T21327
61	62	40.5	40.9	40.9	40.9	300	2	T24292
62	63	40.5	40.9	40.9	40.9	312	2	S51440
63	64	40.5	40.9	40.9	40.9	390	2	A13359
64	65	40.5	40.9	40.9	40.9	483	2	D71439
65	66	40.5	40.9	40.9	40.9	483	2	T0091
66	67	40.5	40.9	40.9	40.9	489	1	S36390
67	68	40.5	40.9	40.9	40.9	498	2	HW85190
68	69	40.5	40.9	40.9	40.9	532	1	CPBY2
69	70	40.5	40.9	40.9	40.9	548	2	T52556
70	71	40.5	40.9	40.9	40.9	576	2	T38665
71	72	40.5	40.9	40.9	40.9	640	2	S52047
72	73	40.5	40.9	40.9	40.9	645	2	T32820
73	74	40.5	40.9	40.9	40.9	707	2	T2127
74	75	40.5	40.9	40.9	40.9	891	2	T30812
75	76	40.5	40.9	40.9	40.9	1166	2	T29090
76	77	40.5	40.9	40.9	40.9	1171	2	T03080
77	78	40.5	40.9	40.9	40.9	1239	1	VHWRVE
78	79	40.5	40.9	40.9	40.9	1240	1	VHWRVE
79	80	40.5	40.9	40.9	40.9	1241	2	S26373
80	81	40.5	40.9	40.9	40.9	1242	2	A56500
81	82	40.5	40.9	40.9	40.9	1242	2	S72350
82	83	40.5	40.9	40.9	40.9	1665	2	T29300
83	84	40.5	40.9	40.9	40.9	2004	2	AC0314
84	85	40.5	40.9	40.9	40.9	2149	2	C96695
85	86	40.5	40.9	40.9	40.9	405	2	T41712
86	87	40.5	40.9	40.9	40.9	732	2	T00130
87	88	40.5	40.9	40.9	40.9	130	2	S31562
88	89	40.5	40.9	40.9	40.9	232	2	AH0252
89	90	40.5	40.9	40.9	40.9	268	2	C90484
90	91	40.5	40.9	40.9	40.9	291	2	GW82135
91	92	40.5	40.9	40.9	40.9	395	2	T24978
92	93	40.5	40.9	40.9	40.9	395	2	G71414
93	94	40.5	40.9	40.9	40.9	395	2	T21089
94	95	40.5	40.9	40.9	40.9	326	1	VGXKRR
95	96	40.5	40.9	40.9	40.9	402	2	T24978
96	97	40.5	40.9	40.9	40.9	407	2	G71414
97	98	40.5	40.9	40.9	40.9	439	2	T28395
98	99	40.5	40.9	40.9	40.9	455	1	T28395
99	100	40.5	40.9	40.9	40.9	466	2	T28395
100	101	40.5	40.9	40.9	40.9	476	2	T49079
101	102	40.5	40.9	40.9	40.9	482	2	T49079



**RESULT 4**

S09334 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C;Species: Sub scrofa domestica (domestic pig)  
 C;Accession: S09334  
 A;Title: Isolation and characterization of a cDNA encoding porcine gastric haptocorrin.  
 A;Reference number: S09334; MUID:90235848; PMID:2331993  
 A;Accession: S09334  
 A;Molecule type: mRNA  
 A;Residues: 1-416 <HEW>  
 A;Cross-references: UNIPROT:P17630; EMBL:X52566; NID:91963; PID:CAA36800.1; PID:g1964  
 C;Superfamily: gastric intrinsic factor  
 C;Keywords: glycoprotein  
 F;1-254/Domain: signal sequence (fragment) #status predicted <SIG>  
 F;25-416/Product: haptocorrin #status predicted <MTS>  

Query Match      48 5%; Score 48; DB 2; Length 416;  
 Best Local Similarity 44.4%; Pred. No. 6.3;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      1 SSDGLWNNOQTQLFLEHS 18  
 Db      378 SVQGTVWANNERTVWEHS 395

**RESULT 5**

JQ1978  
 N;contains: structural polyprotein - Venezuelan equine encephalitis virus (subtype II, strain Everglades)  
 C;Species: Venezuelan equine encephalitis virus  
 C;Accession: JQ1978  
 A;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
 R;Sneider, J.M.; Kinney, R.M.; Tsuchiya, K.R.; Trent, D.W.  
 J. Gen. Virol. 74, 519-523, 1993  
 A;Title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB virus  
 A;Reference number: JQ1978; MUID:93187617; PMID:8445371  
 A;Accession: JQ1978  
 A;Molecule type: mRNA  
 A;Residues: 1-1254 <SNE>  
 C;Cross-references: UNIPROT:P36330; GB:104598; NID:9290612; PID:AAA42984.1; PID:g290614  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-274/Product: coat protein #status predicted <CTP>  
 F;275-333/Product: membrane glycoprotein E3 #status predicted <NG3>  
 F;334-756/Product: membrane glycoprotein E2 #status predicted <NG2>  
 F;701-721/Domain: transmembrane #status predicted <TM1>  
 F;757-812/Product: 6K protein #status predicted <KP6>  
 F;794-813/Domain: transmembrane #status predicted <TM2>  
 F;813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1233-1248/Domain: transmembrane #status predicted <TM3>  
 F;47,285,545,651,946/Binding site: carbohydrate (Asn) (covalent) #status predicted  

Query Match      48 5%; Score 48; DB 1; Length 1254;  
 Best Local Similarity 57.9%; Pred. No. 21;  
 Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Qy      1 SSDGLWNNOQTQLFLE 15  
 Db      762 SLDHLWNNOQMFWTQLLI 780

**RESULT 6**

VHWWVTT  
 N;contains: structural polyprotein - Venezuelan equine encephalitis virus (strain TRD)  
 C;Species: Venezuelan equine encephalitis virus  
 C;Accession: B31467  
 A;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C;Accession: B31467; A47612  
 R;Kinney, R.M.; Johnson, B.J.B.; Brown, V.L.; Trent, D.W.  
 Virology, 152, 400-413, 1986  
 A;Title: The full-length nucleotide sequences of the virulent Trinidad donkey strain of R;Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Tsuchiya, K.R.; Trent, D.W.  
 Virology, 170, 19-30, 1989  
 A;Title: The full-length nucleotide sequences of the virulent Trinidad donkey strain of R;Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Tsuchiya, K.R.; Trent, D.W.  
 A;Reference number: A31467; MUID:89243175; PMID:2524126  
 A;Accession: B31467  
 A;Molecule type: mRNA  
 A;Residues: 1-1254 <K1I>  
 A;Cross-references: UNIPROT:P09592; GB:J04332; NID:9323708; PID:AAB02519.1; PID:g323710  
 R;Kinney, R.M.; Johnson, B.J.B.; Brown, V.L.; Trent, D.W.  
 Virology, 152, 400-413, 1986  
 A;Title: Nucleotide sequence of the 26 S mRNA of the virulent Trinidad donkey strain of R;Kinney, R.M.; Johnson, B.J.B.; Brown, V.L.; Trent, D.W.  
 A;Reference number: A47612; MUID:86263392; PMID:308830  
 A;Accession: A47612  
 A;Molecule type: mRNA  
 A;Residues: 1-542, 'K', 544-810, 'P', 812-1254 <K1I>  
 A;Cross-references: GB:01442  
 C;Superfamily: togavirus structural polyprotein  
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F;1-275/Product: coat protein #status predicted <CTP>  
 F;276-334/Product: membrane glycoprotein E3 #status predicted <NG3>  
 F;335-757/Product: membrane glycoprotein E2 #status predicted <NG2>  
 F;701-718/Domain: transmembrane #status predicted <TM1>  
 F;758-812/Product: 6K protein #status predicted <KP6>  
 F;774-790/Domain: transmembrane #status predicted <TM2>  
 F;795-813/Domain: transmembrane #status predicted <TM3>  
 F;813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>  
 F;1231-1248/Domain: transmembrane #status predicted <TM4>  
 F;47,286,546,652,946/Binding site: carbohydrate (Asn) (covalent) #status predicted  

Query Match      48 5%; Score 48; DB 1; Length 1254;  
 Best Local Similarity 50.0%; Pred. No. 21;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 SSDGLWNNOQTQLFLE 16  
 Db      763 SLDHLWNNOQMFWTQLI 778

RESULT 8  
B44213 structural polyprotein - Venezuelan equine encephalitis virus (strain P676) DNA (cytosine-5-) -methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana  
C;Species: Venezuelan equine encephalitis virus (strain P676)  
N;Alternate name: protein T6G15.160  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: B44213  
R;Kinney, R.M.; Tauchira, K.R.; Sneider, J.M.; Trent, D.W.  
Virology 191, 569-580, 1992  
A;Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses ma  
A;Reference number: A44213; MUID:93079859; PMID:1446915  
A;Accession: B44213  
A;Molecule type: genomic RNA  
A;Residues: 1-1255 <KIN>  
A;Cross-references: UNIPROT:P36322; GB:L04653; NID:9290609; PIDN: AAC19319.1; PID:9290611  
C;Superfamily: togavirus structural polyprotein  
F1-275/Product: coat protein #status predicted <CTP>  
F1-276-334/Product: membrane glycoprotein E3 #status predicted <MG3>  
F1-335-737/Product: membrane glycoprotein E2 #status predicted <MG2>  
F1-702-722/Domain: transmembrane #status predicted <TM1>  
F1-758-813/Product: 6K protein #status predicted <KP6>  
F1-914-1255/Product: membrane glycoprotein E1 #status predicted <MG1>  
F1-1232-1249/Domain: transmembrane #status predicted <TM2>  
F1-47, 286, 652, 947/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match  
Best Local Similarity 48.5%; Score 48; DB 1; Length 1255;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 SDGIGIWNNOTQTLIE 16  
Db 763 SLDHLWNWNQCMFWIQ 778  
RESULT 9  
D44213 structural polyprotein - Venezuelan equine encephalitis virus (strain 3880)  
C;Species: Venezuelan equine encephalitis virus  
C;Accession: D44213  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
R;Kinney, R.M.; Tauchira, K.R.; Sneider, J.M.; Trent, D.W.  
Virology 191, 569-580, 1992  
A;Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses ma  
A;Reference number: A44213; MUID:93079859; PMID:1446915  
A;Accession: D44213  
A;Molecule type: genomic RNA  
A;Residues: 1-1255 <KIN>  
A;Cross-references: UNIPROT:P36322; GB:L00930; NID:9323706; PIDN: AAC19325.1; PID:9137509  
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F1-276-334/Product: coat protein #status predicted <CTP>  
F1-335-737/Product: membrane glycoprotein E3 #status predicted <MG3>  
F1-702-722/Domain: transmembrane #status predicted <TM1>  
F1-758-813/Product: 6K protein #status predicted <KP6>  
F1-795-814/Domain: transmembrane #status predicted <TM2>  
F1-914-1249/Domain: membrane glycoprotein E1 #status predicted <MG1>  
F1-1232-1249/Domain: transmembrane #status predicted <TM2>  
F1-47, 286, 652, 947/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match  
Best Local Similarity 48.5%; Score 48; DB 1; Length 1255;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 SDGIGIWNNOTQTLIE 16  
Db 763 SLDHLWNWNQCMFWIQ 778

RESULT 10  
T06663 DNA (cytosine-5-) -methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana  
N;Alternate name: protein T6G15.160  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Accession: T06663  
R;Stevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X  
submitted to the Protein Sequence Database, April 1999  
A;Reference number: Z15791  
A;Accession: T06663  
A;Molecule type: DNA  
A;Residues: 1-1404 <BEV>  
A;Cross-references: UNIPROT:Q9T011; EMBL:AL049656; GSPDB:GN00062; ATSP:T6G15.160  
A;Experimental source: cultivar Columbia; BAC clone T6G15  
C;Genetics:  
A;Gene: AISP-T6G15.160  
A;Map position: 4  
A;Intron(s): 57/1; 348/3; 371/2; 872/3; 927/3; 989/1; 1026/2; 1086/3; 1152/3; 1245/3; 1288/  
C;Keywords: methyltransferase; S-adenosylmethionine  
Query Match  
Best Local Similarity 47.5%; Score 47; DB 2; Length 1404;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 SDGLMNNTNOTQFL 15  
Db 1095 SDGSWSKQQCQML 1108  
RESULT 11  
S46008 probable carboxypeptidase C (EC 3.4.16.5) YBR139w - Yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YBR1015; hypothetical protein YBR139w  
C;Species: Saccharomyces cerevisiae  
C;Accession: S46008; S46581  
R;Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagalski, M.  
Submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45995  
A;Accession: S46008  
A;Molecule type: DNA  
A;Residues: 1-508 <BBC>  
A;Cross-references: UNIPROT:P38109; EMBL:Z236008; NID:9536435; PIDN:CAA85097.1; PID:9536454;  
A;Experimental source: strain S288C  
R;Becam, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,  
Yeast 10 (Suppl. A), S1-S11, 1994  
A;Title: The sequence of 29.7-kb from the right arm of chromosome II reveals 13 complete c  
A;Reference number: S46569; MUID:94378717; PMID:8091856  
A;Accession: S46569  
A;Molecule type: DNA  
A;Residues: 1-508 <BBC>  
A;Cross-references: EMBL:X75891; NID:9496856; PIDN:CAA53497.1; PID:9496869  
A;Experimental source: strain S288C  
C;Genetics:  
A;Cross-references: SGD:S0000343  
A;Map position: 2R  
A;Note: MIPS\_YBR139w  
C;Superfamily: Serine carboxypeptidase  
C;Keywords: hydrolase; serine carboxypeptidase; transmembrane protein  
F1-22/Domain: transmembrane #status predicted <TM>  
F1-47, 415, 474/Active site: Ser, Asp, His #status predicted  
Query Match  
Best Local Similarity 46.5%; Score 46; DB 1; Length 508;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 WNNNTNOTQFL 16  
Db 160 WNNNNSMIFL 170  
RESULT 12

A86455 unknown protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: A86455  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.E.; Hughes, B.; Huijar, L.  
*Nature* 408, 816-820, 2000  
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, H.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, R.; Rooney, T.; Rowley, D.; Sakano, H.  
 Rizzo, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: A86445  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-230 <SST>  
 A;Cross-references: UNIPROT:Q9C6X3; GB:AE005172; NID:g10092437; PIDN:AAG12841.1; GSPDB:c  
 C;Genetics:  
 C;Map position: 1

**RESULT 13**  
 LNRT2  
 hepatic lectin 2 - rat  
 N;Alternate name: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 31-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 09-Jul-2004  
 C;Accession: B28462; A28462; A31601; A26888; A53417  
 R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.  
*J. Biol. Chem.* 262, 9828-9838, 1987  
 J;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independent of reference number: A28462; MUID:8725056; PMID:3597443  
 A;Accession: B28462  
 A;Cross-references: UNIPROT:P08290; GB:J02762; NID:g205162; PIDN:AA41522.1; PID:g205163  
 A;Residues: 1-301 <HAL>  
 A;Molecule type: mRNA  
 A;Molecule type: mrNA  
 A;Residue: 1-301 <SAN>  
 A;Cross-references: GB:X07636; NID:g57066; PIDN:CNA30476.1; PID:g57067  
 A;Mol. Cell. Biol. 7, 1841-1847, 1987  
 R;McPhee, M.; Berg, P.  
 R;Sanford, J.P.; Elliott, R.W.; Doyle, D.  
*DNA* 7, 721-728, 1988  
 A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.  
 A;Reference number: A31601; MUID:8970119; PMID:3234778  
 A;Accession: A31601  
 A;Cross-references: UNIPROT:P08290; GB:J02762; NID:g205162; PIDN:AA41522.1; PID:g205163  
 A;Residue: 1-301 <SAN>  
 A;Cross-references: GB:X07636; NID:g57066; PIDN:CNA30476.1; PID:g57067  
 A;Molecule type: mRNA  
 A;Molecule type: mrNA  
 A;Title: Identification and characterization of cDNA clones encoding two homologous proteins  
 A;Accession number: A26888; MUID:8725056; PMID:3606447  
 A;Cross-references: GB:ML6347; NID:g906648; PIDN:AA42038.1; PID:g906649  
 A;Residues: 1-122, 'A', 154-201, 'I', 203-259, 'C', 261-301 <MCB>  
 A;Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue 292  
 A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evidence  
 A;Reference number: A25417; MUID:84111554; PMID:6319386

Query Match 45.5%; Score 45; DB 1; Length 301;  
 Best Local Similarity 72.7%; pred. No. 13;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 SDGLWMNNQTO 12  
 Db 276 SDGLWMNDNFQO 286

RESULT 14

S29159

Glutamate receptor, NMDA-sensitive, epsilon-1 chain precursor - mouse

C;Species: Mus musculus (house mouse)  
 C;Date: 11-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: S29159

R;Meguro, H.; Mori, H.; Araki, K.; Kushiyama, E.; Kubuwada, T.; Yamazaki, M.; Kumanishi, Nature 357, 70-74, 1992

A;Title: Functional characterization of a heteromeric NMDA receptor channel expressed from A;Reference number: S29159; MURD:92244361; PMID:1374164

A;Accession: S29159

A;Molecule type: mRNA

A;Residues: 1-1464 <MEG>

A;Cross-references: UNIPROT:P35436; EMBL:D10217; NID:9220410; PID:BA01069.1; PID:922041

C;Superfamily: N-methyl-D-aspartate receptor 2A; glutamate receptor homology  
 C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein

F;1-19/Domain: Signal Sequence #status predicted <SIG>

F;20-1464/Product: glutamate receptor epsilon-1 chain #status predicted <MAT>

F;428-854/Domain: glutamate receptor homology <GRH>

F;557-576/Domain: transmembrane #status predicted <TM1>

F;593-618/Domain: transmembrane #status predicted <TM2>

F;629-647/Domain: transmembrane #status predicted <TM3>

F;811-837/Domain: transmembrane #status predicted <TM4>

Query Match 45.5%; Score 45; DB 1; Length 1464;  
 Best Local Similarity 47.1%; pred. No. 76;  
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SSDGLWMNNQTOFLFH 17  
 Db 1174 NEDGLPNNDQKLYAKH 1190

RESULT 15

A43274

N-methyl D-aspartate receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004

C;Accession: A43274; A45219

R;Monyer, H.; Spruston, R.; Schoepfer, R.; Herb, A.; Higuchi, M.; Lomeli, H.; Burnashev, Science 266, 1217-1221, 1992

A;Title: Heteromeric NMDA receptors: molecular and functional distinction of subtypes.

A;Reference number: A43274; MUID:92271257; PMID:1350383

A;Accession: A43274

A;Molecule type: DNA,  
 A;Residues: 1-1464 <MON>

A;Cross-references: UNIPROT:Q00959; GB:W91561; NID:92905805; PIDN:ACC03565.1; PID:929058C

A;Experimental source: brain  
 A;Note: sequence modified after extraction from NCBI backbone

R;Ishii, T.; Mochizuki, K.; Sugihara, H.; Sakurai, K.; Kadotani, H.; Yokoi, M.; Akazawa, J. Biol. Chem. 268, 2836-2843, 1993

A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor subunits. A;Reference number: A43274; MUID:93155102; PMID:8428958

A;Accession: A45219  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-245, 'F', 247-757, 'T', 759-1464 <ISH>  
A;Cross-references: GB:D13211; NID:9286233; PIDN:BAA02498.1; PID:g286234  
A;Experimental source: brain  
A;Note: sequence extracted from NCBI backbone (NCBIP-12422)  
C;Superfamily: N-methyl-D-aspartate receptor homology <GRH>  
C;428-854/Domain: glutamate receptor homology <GRH>

Query Match Best Local Similarity 45.5%; Score 45; DB 2; Length 1464;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 16  
A22476 muscarinic acetylcholine receptor M4 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C;Accession: A22476  
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seuburg, P.H.  
Biochem. Biophys. Res. Commun. 149, 125-132, 1987  
A;Title: A novel subtype of muscarinic receptor identified by homology screening.  
A;Reference number: A22476; MUID:88077068; PMID:3120722  
A;Accession: A22476  
A;Molecule type: mRNA  
A;Residues: 1-589 <PER>  
A;Cross-references: UNIPROT:P08483; GB:M18088; NID:9202657; PIDN:CAA40659.1; PID:g202658  
A;Experimental source: brain  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F;67-90/Domain: transmembrane #status predicted <TM1>  
F;104-124/Domain: transmembrane #status predicted <TM2>  
F;142-163/Domain: transmembrane #status predicted <TM3>  
F;184-206/Domain: transmembrane #status predicted <TM4>  
F;230-251/Domain: transmembrane #status predicted <TM5>  
F;492-512/Domain: transmembrane #status predicted <TM6>  
F;527-545/Domain: transmembrane #status predicted <TM7>  
P;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted  
P;67-90/Domain: transmembrane #status predicted <TM1>  
P;104-124/Domain: transmembrane #status predicted <TM2>  
P;184-206/Domain: transmembrane #status predicted <TM4>  
P;230-251/Domain: transmembrane #status predicted <TM5>  
P;492-512/Domain: transmembrane #status predicted <TM6>  
P;527-545/Domain: transmembrane #status predicted <TM7>

Query Match Best Local Similarity 44.4%; Score 44; DB 2; Length 589;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

RESULT 17  
S10128 muscarinic acetylcholine receptor M4 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10128  
R;Paralita, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression  
A;Reference number: S04326; MUID:8816632; PMID:3443095  
A;Accession: S10128  
A;Molecule type: DNA  
A;Residues: 1-590 <PER>  
A;Cross-references: UNIPROT:P20309; EMBL:X15266; NID:932323; PIDN:CAA33337.1; PID:g32324  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane  
F;65-95/Domain: transmembrane #status predicted <TM1>  
F;105-131/Domain: transmembrane #status predicted <TM2>  
F;143-164/Domain: transmembrane #status predicted <TM3>  
F;185-207/Domain: transmembrane #status predicted <TM4>  
F;221-222/Domain: transmembrane #status predicted <TM5>  
F;493-513/Domain: transmembrane #status predicted <TM6>  
F;525-546/Domain: transmembrane #status predicted <TM7>  
F;5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted  
P;6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted  
P;67-90/Domain: transmembrane #status predicted <TM1>  
P;104-124/Domain: transmembrane #status predicted <TM2>  
P;184-206/Domain: transmembrane #status predicted <TM4>  
P;230-251/Domain: transmembrane #status predicted <TM5>  
P;492-512/Domain: transmembrane #status predicted <TM6>  
P;527-545/Domain: transmembrane #status predicted <TM7>

Query Match Best Local Similarity 44.4%; Score 44; DB 2; Length 590;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

RESULT 18  
QY 1 SSDGLWNNNQTQLEHS 18  
Db 331 SSSDSWNNDAAASLENS 348

Query Match Best Local Similarity 50.0%; Score 40; DB 2; Length 589;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

RESULT 19  
S0114 muscarinic acetylcholine receptor M2, glandular - pig  
N;Alternate names: muscarinic acetylcholine receptor III  
C;Species: Sus scrofa domesticus (domestic pig)  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C;Accession: S0114  
R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.  
A;Molecule type: mRNA  
A;Accession: B94518  
A;Reference number: A94518  
A;Cross-references: UNIPROT:P08483  
R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Braun, M.R.  
Science 237, 527-532, 1987  
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.  
A;Reference number: A94293; MUID:87263421; PMID:3037705  
A;Accession: B94293  
A;Molecule type: mRNA  
A;Residues: 1-269; 463-589 <BO2>

A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist A;Reference number: S0114; MUID:88296835; PMID:3402600  
A;Molecule type: DNA  
A;Accession: 1-930 <AKT>  
A;Cross-references: UNIPROT:P11483; EMBL:X12712; NID:91861; PIDN:CAA31215.1; PID:91862  
C;Superfamily: vertebrate Rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane receptor; transmembrane #status predicted <TM1>  
F;68-91/Domain: transmembrane #status predicted <TM2>  
F;105-125/Domain: transmembrane #status predicted <TM3>  
F;143-164/Domain: transmembrane #status predicted <TM4>  
F;185-207/Domain: transmembrane #status predicted <TM5>  
F;231-252/Domain: transmembrane #status predicted <TM6>  
F;493-513/Domain: transmembrane #status predicted <TM7>  
F;528-546/Domain: transmembrane #status predicted <TM8>  
Query Match Similarity 44.4%; Score 44; DB 2; Length 590;  
Best Local Similarity 50.0%; Pred. No. 40; Mismatches 1; Indels 0; Gaps 0;  
Matches 9; Conservative 1; MisMatches 8; Indels 0; Gaps 0;  
Qy 1 SSDGLWMNNQTLFLEHS 18  
Db 332 SSSDSWMNDAASLENS 349

RESULT 20  
S47572  
muscarinic acetylcholine receptor m3 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S47572  
R;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
Biochim. Biophys. Acta 1233, 151-154, 1994  
A;Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 receptor  
A;Reference number: S47572; MUID:94339178; PMID:8061048  
A;Accession: S47572  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-590 <JEB>  
A;Cross-references: UNIPROT:P41984; EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:95204  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: neurotransmitter receptor  
C;Keywords: neurotransmitter receptor

Query Match Similarity 44.4%; Score 44; DB 2; Length 590;  
Best Local Similarity 50.0%; Pred. No. 40; Mismatches 1; MisMatches 8; Indels 0; Gaps 0;  
Matches 9; Conservative 1; MisMatches 8; Indels 0; Gaps 0;  
Qy 1 SSDGLWMNNQTLFLEHS 18  
Db 332 SSSDSWMNDAASLENS 349

RESULT 21  
A55019  
muscarinic acetylcholine receptor, M3 isoform - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A55019  
R;Grobut, A.P.; Galper, J.B.  
J. Biol. Chem. 269, 25823-25829, 1994  
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
A;Reference number: A55019; MUID:95014393; PMID:7929287  
A;Accession: A55019  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-639 <GAD>  
A;Cross-references: UNIPROT:P49578; GB:LI0617; NID:9530097; PIDN:AAA65961.1; PID:9530098  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: neurotransmitter receptor

Query Match Similarity 44.4%; Score 44; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 44; Mismatches 9; Conservative 1; MisMatches 8; Indels 0; Gaps 0;  
Matches 9; Conservative 1; MisMatches 8; Indels 0; Gaps 0;

RESULT 22

QY	1.	SSDQIWNNTQTLFLEHS	18
C.Species:	Streptomyces coelicolor		
C.Date:	05-Nov-1999	#sequence_revision	05-Nov-1999 #text_change 09-Jul-2004
C.Accession:	T35238		
R.Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.			
submitted to the EMBL Data Library, September 1998			
A;Accession:	T35238		
A;Status:	preliminary;	translated from	GB/EMBL/DDBJ
A;Molecule type:	DNA		
A;Cross-references:	UniProt:O86728; EMBL:AL031515; PMID:CAA20643.1; GSPDB:GN00070; SCOEDB		
A;Experimental source:	strain A3(2)		
A;Genetics:			
A;Gene:	SCOEDB:SC5CC7.31c		

Query Match      Score 44; DB 2; Length 973;  
 Best Local Similarity 63.6%; Pred. No. 70; Mismatches 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 1;

Qy	3	DGHWNNNOTOL 13
Db	872	DGHWNNNDAL 882

RESULT 23

GBCE	beta-galactosidase (EC 3.2.1.23) alpha chain - Escherichia coli (strain K-12)
N;Alternate names:	beta-D-galactoside galactohydrolyase; lactase; phospho-beta-D-galactos
C.Species:	Escherichia coli
C.Date:	30-Sep-1987 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004
C.Accession:	A65096; H25751; S020206
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co	
A.; Rose, D.J.; Mau, B.; Shao, Y.	
Science 277, 1455-1462, 1997	
A;Title:	The complete genome sequence of Escherichia coli K-12.
A;Reference number:	A64720; MUID:97426617; PMID:9278503
A;Accession:	A65096
A;Status:	nucleic acid sequence not shown; translation not shown
A;Molecule type:	DNA
A;Residues:	1-1042 <BLAT>
A;Cross-references:	UniProt:P06664; UniProt:Q41170; GB:AB000389; GB:U000096; NID:91789451
A;Experimental source:	strain K-12, sub-strain MG1655
R;Stokes, H.W.; Betts, P.W.; Hall, B.G.	
Mol. Biol. Evol. 2, 469-477, 1985	
A;Title:	Sequence of the ebgA gene of Escherichia coli: comparison with the lacZ gene.
A;Reference number:	A93056; MUID:88216133; PMID:393707
A;Accession:	A25751
A;Molecule type:	DNA
A;Residues:	80-476, 'R', 478-651, 'S', 653-660, 'P', 662-674, 'CRSWIPAKRS', 685-724, 'KCASV', 730-
A;Cross-references:	GB:X03228; GB:MI13700; GB:MI13796; NID:941311; PMID:CAA26978.1; PID:94
R;Fowler, A.V.; Smith, P.J.	
J. Biol. Chem. 258, 10204-10207, 1983	
A;Title:	The active site regions of lacZ and ebg beta-galactosidases are homologous.
A;Reference number:	A92390; MUID:8329032; PMID:6411710
A;Contents:	annotation; active site regions
R;Hall, B.G.; Betts, P.W.; Wootten, J.C.	
Genetics 123, 635-648, 1989	
A;Title:	DNA sequence analysis of artificially evolved ebg enzyme and ebg repressor gene
A;Reference number:	S09205; MUID:90128218; PMID:2515108
A;Accession:	S09206
A;Molecule type:	DNA
A;Residues:	13-476, 'R', 478-651, 'S', 653-660, 'P', 662-779, 'M', 780-1037, 'T', 1039-1042 <HAL>
A;Cross-references:	EMBL:X52031; NID:941307; PID:CAA36274.1; PID:941309
C;Comment:	The wild-type enzyme is an ineffective lactase. Two classes of point mutation:

C;Genetics:  
A;Gene: ebga  
A;Map position: 68 min  
C;Complex: homohexamer  
C;Superfamily: beta-galactosidase  
C;Keywords: glycosidase; hexamer; hydrolase; magnesium  
F:413';415,461;Binding site: Glu, His, Glu) #status predicted  
P:461,502,524/Active site: Glu, Tyr, Glu #status predicted

Query Match 44.4%; Score 44; DB 1; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLRH 17  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 24  
B85668 evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain 0157:H7)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B85668  
R;Perma\_N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, R.; Glass, J.I.; Leffkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chan, E.Y.; Cassell, G.H.  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: B85668  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1042 <STO>  
A;Cross-references: UNIPROT:Q8XAM9; GB:AE005174; NID:912517660; PIDN:AAG58209.1; GSPDB:Q  
A;Experimental source: strain 0157:H7, substrain EDL033  
C;Genetics:  
A;Gene: ebga  
C;Superfamily: beta-galactosidase

Query Match 44.4%; Score 44; DB 2; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLRH 17  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 25  
F91123 evolved beta-D-galactosidase alpha subunit [imported] - Escherichia coli (strain 0157:H7)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: F91123  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurikawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gabbara, N.; Yabunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genetic reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: F91123  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1042 <HAY>  
A;Cross-references: UNIPROT:Q8XAM9; GB:BA000007; PIDN:BAB37381.1; PIDN:913363431; GSPDB:Q  
A;Experimental source: strain 0157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: EC83958  
C;Superfamily: beta-galactosidase

Query Match 44.4%; Score 44; DB 2; Length 1042;  
Best Local Similarity 46.7%; Pred. No. 76;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLRH 18  
Db 788 EGLWQPNHLQIMQEH 802

RESULT 26  
C82931 hypothetical protein UU126 [imported] - Ureaplasma urealyticum  
C;Species: Ureaplasma urealyticum  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: C82931  
R;Glass, J.I.; Leffkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chan, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor  
A;Reference number: A82870  
A;Accession: C82931  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1084 <GLA>  
A;Cross-references: GB:AE002113; GB:AF222994; NID:96899078; PIDN:AAF30532.1; GSPDB:GN001;  
A;Experimental source: Serovar 3; biovar 1  
C;Genetics:  
A;Gene: UU126  
A;Genetic code: SGCG3  
Query Match 44.4%; Score 44; DB 2; Length 1084;  
Best Local Similarity 50.0%; Pred. No. 79;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNQTQFLRHS 18  
Db 479 LWASQNQNLYLDYS 492

RESULT 27  
S76938 hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 16-Aug-2004  
C;Accession: S76938  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okamura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, S.;  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S76938  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-254 <KAN>  
A;Cross-references: UNIPROT:P74730; EMBL:D90917; GB:AB001339; NID:91653036; PIDN:PA18085C  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Superfamily: ATP-binding cassette homology  
C;Keywords: ATP; nucleotide binding; P-loop  
P:45-25(Domain: nucleotide binding cassette homology <ABC>  
P:62-69/Region: nucleotide binding motif A (P-loop)

Query Match 43.4%; Score 43; DB 2; Length 254;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 DGLMANNNQTQFLRH 18  
Db 193 DKLWQPNHLQIMQEH 208

RESULT 28  
AG2598 conserved hypothetical protein phng [imported] - Agrobacterium tumefaciens (strain C58, 1  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 12-Jul-2004  
C;Accession: AG2598

R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavim, T.; Levy, R.; Li, M.; McClellan, A.; Karp, P.; Romero, P.; Zhang, S.; Science, 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AG2598

A;Status: preliminary

A;Molecule type: DNA

C;Genetics:

A;Residue: 1-153 <KUR>

A;Cross-references: UNIPROT:Q8UTW0; GB:AE008688; PIDN:AAL41205.1; PID:gi17738507; GSPDB:C

Query Match Best Local Similarity 42.4%; Score 42; DB 2; Length 153; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DGLWNNGNTQFLIE 16  
| || :||: |:  
Db 103 DALWQESQTRGPIE 116

RESULT 29

H97380

Query Match Best Local Similarity 50.0%; Score 42; DB 2; Length 153; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DALWQESQTRGPIE 16  
| || :||: |:  
Db 103 DALWQESQTRGPIE 116

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58.

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: H97380

A;Status: preliminary

A;Molecule type: DNA

A;Residue: 1-153 <KUR>

A;Cross-references: UNIPROT:Q8UTW0; GB:AE007869; PIDN:AAKB6001.1; PID:gi15155066; GSPDB:C

C;Genetics:

A;Gene: AGR\_C\_303

A;Map position: circular chromosome

C;superfamily: carbon-phosphorus lyase, component PhnG

Query Match Best Local Similarity 42.4%; Score 42; DB 2; Length 153; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DGLWNNGNTQFLIE 16  
| || :||: |:  
Db 103 DALWQESQTRGPIE 116

RESULT 30

H65067

Query Match Best Local Similarity 50.0%; Score 42; DB 2; Length 153; Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DALWQESQTRGPIE 16  
| || :||: |:  
Db 103 DALWQESQTRGPIE 116

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: AE4720; MUID:97426617; PMID:9278503

A;Accession: H65067

A;Status: preliminary

A;Molecule type: DNA

A;Residue: 1-269 <BLT>

C;Species: Escherichia coli

C;Name: Escherichia coli (strain K-12)

C;Taxonomy ID: 511571

C;Classification: Bacteria

C;Database: 12-Sep-1997 #Sequence\_revision 17-Sep-1997 #Text\_change 09-Jul-2004

R;Blattner, F.R., Plunkett III, G., Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vega, L., Rose, D.J., Mau, B., Shao, Y., Science, 277, 1453-1462, 1997.

A;Cross-references: UNIPROT:Q46942; GB:AE000368; GB:U00096; NID:92367165; PIDN:AACT5986 ..

A;Experimental source: Strain K-12, Substrain MG1655

Query Match 42 4%; Score 42; DB 2; Length 269;  
Best Local Similarity 58.3%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQFFE 16  
Db 173 LWNNQPKPFFK 184

RESULT 31

H91091  
probable sensory transducer [imported] - Escherichia coli (strain 0157:H7, substrain RIMD902021) #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C;Species: Escherichia coli  
C;Accession: H91091  
C;Date: 18-Jul-2001  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with O157:H7 and O104:H4 strains

A;Reference number: A99629; NUID:21156231; PMID:1258796

A;Accession: H91091  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-269 <HAY>  
A;Cross-references: UNIPROT:Q8X6I3; GB:BA000007; PIDN:BAB37127.1; PIDN:g13363176; GSPDB:G  
A;Experimental source: strain 0157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: E863704

Query Match 42 4%; Score 42; DB 2; Length 269;  
Best Local Similarity 58.3%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQFFE 16  
Db 173 LWNNQPKPFFK 184

RESULT 32

C85937  
probable sensory transducer yqeI [imported] - Escherichia coli (strain 0157:H7, substrain RIMD902021) #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Species: Escherichia coli  
C;Accession: C85937  
C;Date: 16-Feb-2001  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoacaca, Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.  
A;Reference number: A85480; NUID:21074935; PMID:11206551  
A;Accession: C85937  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-269 <STO>  
A;Cross-references: UNIPROT:Q8X6I3; GB:AE005174; NID:912517339; PIDN:AAG57959.1; GSPDB:G  
A;Experimental source: strain 0157:H7, substrain EDL933  
C;Genetics:  
A;Gene: yqeI

Query Match 42 4%; Score 42; DB 2; Length 269;  
Best Local Similarity 58.3%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LWNNNOTQFFE 16  
Db 173 LWNNQPKPFFK 184

RESULT 33

S73153  
hypothetical protein 10 - red alga (*Porphyra purpurea*) chloroplast



Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 LWNNTQTLIE 16  
 :||: ||: ||:  
 Db 11 WWDQDTREYLE 22

RESULT 38

A5932 cytochrome C-type biogenesis protein CCW5 - Cyanidioschyzon merolae mitochondrial C;Species: mitochondrial Cyanidioschyzon merolae

C;Accession: A5932 Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004

R;Ohta, N.; Sato, N.; Kuroiwa, T.  
Nucleic Acids Res. 26, 519-519, 1998

A;Title: Structure and organization of the mitochondrial genome of the unicellular red alga Cyanidioschyzon merolae

A;Reference number: A58930; MUID:99030526; PMID:9801318

A;Accession: A58932  
A;Status: preliminary

A;Molecule type: DNA  
A;Cross-references: 1-620 <ARN>

A;Cross-references: UNIPROT:Q9ZZP7; GB:D89861; NID:94115781; PIDN:BA136527.1; PID:941157

C;Genetics:  
A;Gene: yejR; ccmP

A;Genome: mitochondrial  
C;Superfamily: nrnE protein  
C;Keywords: mitochondrial

Query Match 42.4%; Score 42; DB 2; Length 620;  
Best Local Similarity 63.6%; Pred. No. 88; Mismatches 7;  
Matches 7; Conservative 2; Indels 0; Gaps 0;

Qy 5 LWNNTQTLIE 15  
|:||: ||: ||:  
Db 91 LWSNNNEGSLFL 101

RESULT 39

S75724 hypothetical protein slr0907 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S75724 R;Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O., K.; Okumura, S.; Shimpoo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

B;A;Reference number: S74322; MUID:97061201; PMID:8905231.

A;Accession: S75724  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
A;Residues: 1-1014 <KAN>

A;Cross-references: UNIPROT:Q55374; EMBL:D64003; GB:AB001339; NID:91001200; PIDN:BA1045  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 42.4%; Score 42; DB 2; Length 1014;  
Best Local Similarity 43.8%; Pred. No. 1.5e+02; Mismatches 7;  
Matches 7; Conservative 5; Indels 4; Gaps 0;

Qy 1 SSDGLWNNTQTLIE 16  
|:||: ||: ||:  
Db 819 NSHGIWSHTASQLFPE 834

RESULT 40

S72645 pIY1 protein - Pseudomonas aeruginosa

C;Species: Pseudomonas aeruginosa  
C;Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004

C;Accession: S72645; S72633  
R;Alm, R.A.; Hallinan, J.P.; Watson, A.A.; Mattick, J.S.

Submitted to the EMBL Data Library, April 1996  
A;Description: Fimbrial biogenesis genes of *Pseudomonas aeruginosa*: pilW and pilX increase the  
omologue.  
A;Reference number: S72643

A;Accession: S72645  
A;Molecule type: DNA  
A;Residues: 1-1161 <ALM>

A;Cross-references: UNIPROT:Q51536; EMBL:L76605; NID:91246298; PIDN:AAA33502.1; PID:91246

A;Experimental source: strain PAl  
R;Alm, R.A.; Hallinan, J.P.; Watson, A.A.; Mattick, J.S.

Mol. Microbiol. 22, 161-173, 1996

A;Title: Fimbrial biogenesis genes of *Pseudomonas aeruginosa*: pilW and pilX increase the  
omologue.

A;Reference number: S72631; MUID:97055431; PMID:8897918

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA  
A;Residues: 657-913 <ALW>

A;Cross-references: EMBL:L76605

A;Note: only a part of the translation is shown  
A;The nucleotide sequence was submitted to the EMBL Data Library, April 1996

C;Genetics:  
A;Gene: pylV

A;Function: may be involved in assembly of type 4 fimbriae

C;Keywords: fimbria; membrane protein

Query Match 42.4%; Score 42; DB 2; Length 1161;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SDGLWNNTQTL 13  
|:||: ||: ||:  
Db 357 TDGLWNDSAV 368

Search completed: December 30, 2004, 16:13:57  
Job time : 43 secs



OM protein - protein search, using sw model  
 Run on: December 30, 2004, 16:23:09 ; Search time 37 Seconds  
 (without alignments)  
 32.263 Million cell updates/sec

**Title:** US-10-718-321-1  
**Perfect score:** 99  
**Sequence:** 1 SSDGLWNNNNQQLFLEHHS 18

**Scoring table:** BL0SUM62  
**Gapop 10.0 , Gapext 0.5**

**Searched:** 478139 seqs, 66318000 residues

**Total number of hits satisfying chosen parameters:** 187706

**Minimum DB seq length:** 0  
**Maximum DB seq length:** 20

**Post-processing:** Minimum Match 0%  
 Maximum Match 100%  
 Listing first 150 summaries

**Database :**

Issued Patents AA: *	1: /cgn2_6/pctodata/1/1aa/51_COMB.pep:*
2: /cgn2_6/pctodata/1/1aa/5B_COMB.pep:*	
3: /cgn2_6/pctodata/1/1aa/6a_COMB.pep:*	
4: /cgn2_6/pctodata/1/1aa/6B_COMB.pep:*	
5: /cgn2_6/pctodata/1/1aa/potus_COMB.pep:*	
6: /cgn2_6/pctodata/1/1aa/backfile1.pep:*	

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Length	DB ID	Description
1	34	34.3	19	4	US-09-441-502B-68 Sequence 68, Appli
2	32	32.3	12	3	US-09-817-177-2 Sequence 2, Appli
3	32.3	12	5	PCT-US95-12686-2 Sequence 1, Appli	
4	32	32.3	19	1	US-08-218-025A-166. Sequence 166, Appli
5	31	31.3	7	1	US-08-424-957-7 Sequence 22, Appli
6	31	31.3	7	3	US-09-035-686-7 Sequence 7, Appli
7	30	30.3	13	3	US-08-592-500-6 Sequence 7, Appli
8	30	30.3	13	3	US-08-195-006-6 Sequence 6, Appli
9	30	30.3	5	PCT-US94-07644A-6 Sequence 6, Appli	
10	30	30.3	14	4	US-09-638-203-25 Sequence 25, Appli
11	30	30.3	20	1	US-08-218-025A-82 Sequence 82, Appli
12	30	30.3	20	3	US-08-612-973-73 Sequence 73, Appli
13	30	30.3	20	3	US-08-612-973-82 Sequence 6, Appli
14	30	30.3	20	3	US-08-927-597-73 Sequence 6, Appli
15	30	30.3	20	3	US-08-927-597-82 Sequence 6, Appli
16	30	30.3	20	4	US-08-635-886C-38 Sequence 25, Appli
17	30	30.3	20	4	US-08-635-886C-47 Sequence 82, Appli
18	30	30.3	20	4	US-08-635-886C-56 Sequence 73, Appli
19	30	30.3	20	4	US-08-635-886C-56 Sequence 82, Appli
20	30	30.3	20	4	US-08-635-886C-56 Sequence 73, Appli
21	30	30.3	20	4	US-08-974-690C-47 Sequence 73, Appli
22	30	30.3	20	4	US-08-974-690C-56 Sequence 73, Appli
23	30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli
24	30	30.3	20	4	US-09-881-710-17 Sequence 73, Appli
25	30	30.3	20	4	US-08-974-685-47 Sequence 73, Appli
26	30	30.3	20	4	US-08-974-685-56 Sequence 73, Appli
27	30	30.3	20	4	US-08-974-690C-38 Sequence 73, Appli
28	30	30.3	20	4	US-08-974-690C-47 Sequence 73, Appli
29	30	30.3	20	4	US-08-974-690C-56 Sequence 73, Appli
30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli	
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33	30	30.3	20	4	US-08-974-685-56 Sequence 73, Appli
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35	30	30.3	20	4	US-08-974-690C-47 Sequence 73, Appli
36	30	30.3	20	4	US-08-974-690C-56 Sequence 73, Appli
37	30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli
38	30	30.3	20	4	US-09-881-710-17 Sequence 73, Appli
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40	30	30.3	20	4	US-08-974-685-56 Sequence 73, Appli
41	30	30.3	20	4	US-08-974-690C-38 Sequence 73, Appli
42	30	30.3	20	4	US-08-974-690C-47 Sequence 73, Appli
43	30	30.3	20	4	US-08-974-690C-56 Sequence 73, Appli
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98	30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli
99	30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli
100	30	30.3	20	4	US-08-974-710-15 Sequence 73, Appli



COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
 APPLICATION NUMBER: PCT/US95/12686  
 FILING DATE:  
 CLASSIFICATION:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US95-12686-2

Query Match 32.3%; Score 32; DB 5; Length 12;  
 Best Local Similarity 45.5%; Pred. No. 65;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Qy 2 SDGLWNNOOTQ 12  
 Db 1 ASSLWNTNQDQ 11

RESULT 4  
 US-08-218-025A-166  
 Patent No. 556744  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, David B.  
 APPLICANT: Ugen, Kenneth E.  
 APPLICANT: Williams, William V.  
 TITLE OF INVENTION: Methods and Compositions for Diagnosing  
 TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
 NUMBER OF SEQUENCES: 197  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Houston and Houston  
 STREET: P.O. Box 457, 321 No. 555674 Aristostown Road  
 CITY: Spring House  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19477

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 REFERENCE NUMBER: US/08/277,660A  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreicer, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-60244/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 TOPOLOGY: linear  
 US-08-277-660A-22

Query Match 31.3%; Score 31; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 SDGLW 6  
 Db 3 SDGLW 7

RESULT 6  
 US-08-424-957-7  
 Sequence 7, Application US/08424957  
 Patent No. 5770377  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Rohbach, Teet, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco

Query Match 32.3%; Score 32; DB 1; Length 19;

STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 7:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown

US-08-424-957-7

Query Match 31.3%; Score 31; DB 1; length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2 SDGLW 6	
Db	3 SDGLW 7	

RESULT 7

US-09-035-686-7

Sequence 7, Application US/09035686  
 Sequence No. 6, Application US/08592500  
 GENERAL INFORMATION:  
 APPLICANT: Picklesley, Steven M.  
 APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: US  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/592,500  
 FILING DATE:  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/089,455  
 FILING DATE: 09-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Karen B.  
 REGISTRATION NUMBER: 29,684  
 REFERENCE DOCKET NUMBER: 12418-28  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..13  
 OTHER INFORMATION: /note= "K5/6 peptide residues  
 OTHER INFORMATION: 1-13."

US-08-592-500-6

Query Match 30.3%; Score 30; DB 3; Length 13;

REGISTRATION NUMBER: 24,190  
 REFERENCE DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown

US-09-035-686-7

Query Match 31.3%; Score 31; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2 SDGLW 6	
Db	3 SDGLW 7	

RESULT 8

US-08-592-500-6

Sequence 6, Application US/08592500  
 Patent No. 605089  
 GENERAL INFORMATION:  
 APPLICANT: Lanza, Francois  
 APPLICANT: Phillips, David R.  
 APPLICANT: Cazenave, Jean-Pierre  
 TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Khourie and Crew  
 STREET: 379 Luton Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: US  
 ZIP: 94301

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/592,500  
 FILING DATE:  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/089,455  
 FILING DATE: 09-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Karen B.  
 REGISTRATION NUMBER: 29,684  
 REFERENCE DOCKET NUMBER: 12418-28  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..13  
 OTHER INFORMATION: /note= "K5/6 peptide residues  
 OTHER INFORMATION: 1-13."

US-08-592-500-6

Best Local Similarity 71.4%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QLFLEHS 18  
Db 7 QLFIDHN 13

RESULT 9

US-08-195-006-6 Application US/08195006

; Sequence 6, Application PC/TUS9407644A

; GENERAL INFORMATION:

; ; PATENT NO. 608688

; ; APPLICANT: Lanza, Francois

; ; APPLICANT: Phillips, David R.

; ; APPLICANT: Cazenave, Jean-Pierre

; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/195,006

FILING DATE: 10-FEB-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,455

FILING DATE: 09-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 12418-28

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

EMAIL: karen.dow@takata.com

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

NAME/KEY: Peptide

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "K5/6 peptide residues

OTHER INFORMATION: 1-13."

PCT-US94-07644A-6

Query Match Best Local Similarity 71.4%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QLFLEHS 18  
Db 7 QLFIDHN 13

RESULT 11

US-09-638-203-25

; Sequence 25, Application US/09638203

; ; PATENT NO. 660201

; GENERAL INFORMATION:

; ; APPLICANT: Daniel E.H. Afar

; ; APPLICANT: Rene S. Hubert

; ; APPLICANT: Aya Jakobovits

; ; APPLICANT: Arthur B. Rattano

; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE PROTEIN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF

; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF

; FILE REFERENCE: 129\_2005U1

; CURRENT APPLICATION NUMBER: US/09/638,203

; CURRENT FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/148,935

; PRIOR FILING DATE: 1999-08-12

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 25

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo Sapiens

; US-09-638-203-25

Query Match Best Local Similarity 55.6%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QLFLEHS 18  
Db 7 QLFIDHN 13

RESULT 10

PCT-US94-07644A-6

; Sequence 6, Application PC/TUS9407644A

; GENERAL INFORMATION:

; ; APPLICANT: COR Therapeutics, Inc.

; ; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses

; ; NUMBER OF SEQUENCES: 43

Qy 4 GLWNNQTO 12

Db 1 GLWRNGDQ 9  
 RESULT 12  
 US-08-218-025A-82  
 Sequence 82, Application US/08218025A  
 Patent No. 5556744  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, David B.  
 APPLICANT: Ugen, Kenneth E.  
 APPLICANT: Williams, William V.  
 TITLE OF INVENTION: Methods and Compositions for Diagnosing  
 TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
 NUMBER OF SEQUENCES: 197  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Howton and Howton  
 STREET: P.O. Box 47, 321 NO. 5556744ristown Road  
 CITY: Spring House  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19477  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/612,973  
 FILING DATE: 11-MAR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.  
 REGISTRATION NUMBER: 32,205  
 REFERENCE/DOCKET NUMBER: 1487-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4100  
 TELEFAX: (703) 816-4100  
 INFORMATION FOR SEQ ID NO: 73:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-612-973-73  
 Query Match 30.3%; Score 30; DB 1; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 2.4e+02; Indels 0;  
 Matches 5; Conservative 4; Mismatches 4; Gaps 0;  
 Qy 1 SSDGILWNNTQL 13  
 Db :::::|:|:| 7 NTNGQWHINSTAL 19  
 RESULT 14  
 US-08-612-973-82  
 Sequence 82, Application US/08612973  
 Patent No. 6150134  
 GENERAL INFORMATION:  
 APPLICANT: MARTEENS, GEERT  
 APPLICANT: BOSMAN, FONS  
 APPLICANT: DE MARTYNOFF, GUY  
 APPLICANT: BUYSE, MARIE-ANGE  
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/612,973  
 FILING DATE: 11-MAR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.  
 REGISTRATION NUMBER: 32,205  
 REFERENCE/DOCKET NUMBER: 1487-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4100  
 TELEFAX: (703) 816-4100  
 Query Match 30.3%; Score 30; DB 1; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 2.4e+02; Indels 0;  
 Matches 4; Conservative 1; Mismatches 1; Gaps 0;  
 Qy 3 DGLWNN 8  
 Db 1 DDIWN 6  
 RESULT 13  
 US-08-612-973-73  
 Sequence 73, Application US/08612973  
 Patent No. 6150134  
 GENERAL INFORMATION:  
 APPLICANT: MAERTENS, GEERT  
 APPLICANT: BOSMAN, FONS  
 APPLICANT: DE MARTYNOFF, GUY  
 APPLICANT: BUYSE, MARIE-ANGE  
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
 TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/612,973  
 FILING DATE: 11-MAR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.  
 REGISTRATION NUMBER: 32,205  
 REFERENCE/DOCKET NUMBER: 1487-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4100  
 TELEFAX: (703) 816-4100

## INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

US-08-927-597-82

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-612-973-82

Query Match

Best Local Similarity

Score 30;

DB 3;

Length 20;

Matches

4; Conservative

Pred. No. 2.4e+02;

2; Mismatches

4;

Indels

0;

Gaps

0;

Qy

6

WNNNOTQFL

15

| : | : | : |

Db

7

WGENDTDVFV

16

RESULT 15

US-08-927-597-73

Sequence 73, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: DE MARTYNOFF, GUY

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,597

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

RESULT 16

US-08-927-597-82

Sequence 82, Application US/08927597

Patent No. 6245503

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: DE MARTYNOFF, GUY

APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHVE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,597

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-927-597-82

RESULT 17

US-08-635-886C-38

Sequence 38, Application US/08635886C

Patent No. 6555114

GENERAL INFORMATION:

APPLICANT: LEROUX-ROBLIS, Geert

APPLICANT: DELYS, Robert

APPLICANT: MAERTENS, Geert

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C VIRUS

FILE REFERENCE: 2752-18

CURRENT APPLICATION NUMBER: US/08/635,886C

CURRENT FILING DATE: 1996-04-25

PRIOR APPLICATION NUMBER: PCT/EP94/03555

PRIOR FILING DATE: 1994-10-28

PRIOR APPLICATION NUMBER: EP 93402718.6

Query Match

Best local Similarity

Score 30;

DB 3;

Length 20;

Matches

5; Conservative

Pred. No. 2.4e+02;

2; Mismatches

4;

Indels

0;

Gaps

0;

Qy

1

SDGLWNNNOTQQL

13

| : | : | : |

Db

7

NTNGQWHINSTAL

19

US-08-927-597-73

Query Match

Best local Similarity

Score 30;

DB 3;

Length 20;

Matches

4; Conservative

Pred. No. 2.4e+02;

2; Mismatches

4;

Indels

0;

Gaps

0;

Qy

6

WNNNOTQFL

15

| : | : | : |

Db

7

WGENDTDVFV

16

US-08-927-597-82

```

; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-38

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.4e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15
Db 7 WGENDTDVFPV 16

RESULT 18
US-08-635-886C-47
; Sequence 47, Application US/08635886C
; Patient No: 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-47

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.4e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDGIWNNNOTQL 13
Db 7 NTNGSWHINSTAL 19

RESULT 19
US-08-635-886C-56
; Sequence 56, Application US/08635886C
; Patient No: 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 56
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-56

Query Match 30.3%; Score 30; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.4e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFL 15
Db 7 WGENDTDVFPV 16

```

RESULT 21  
US-08-974-690C-47  
; Sequence 47, Application US/08974690C  
; Patent No. 661333  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELETS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C VIRUS  
; FILE REFERENCE: 2251-94  
; CURRENT APPLICATION NUMBER: US/08/974,690C  
; CURRENT FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
; US-08-974-690C-47

RESULT 22  
US-08-974-690C-55  
; Sequence 55, Application US/08974690C  
; Patent No. 661333  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELETS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C VIRUS  
; FILE REFERENCE: 2251-94  
; CURRENT APPLICATION NUMBER: US/08/974,690C  
; CURRENT FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
; US-08-974-690C-56

RESULT 23  
US-09-881-710-15  
; Sequence 15, Application US/09881710  
; Patent No. 6673895  
; GENERAL INFORMATION:  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 209671US0  
; CURRENT APPLICATION NUMBER: US/09/881,710  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
; US-09-881-710-15

RESULT 24  
US-09-881-710-17  
; Sequence 17, Application US/09881710  
; Patent No. 6673895  
; GENERAL INFORMATION:  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 209671US0  
; CURRENT APPLICATION NUMBER: US/09/881,710  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 30

LOCATION: (6) .. (6)  
; OTHER INFORMATION: Xaa is Ile or Val  
; FEATURE: ..  
; NAME/KEY: MISC FEATURE  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: Xaa is Thr or Ser  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (14)..(14)  
; OTHER INFORMATION: Xaa is Leu or Ile  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (16)..(16)  
; OTHER INFORMATION: Xaa is Ser or Arg  
; US-09-881-710-15  
; Sequence 15, Application US/09881710  
; Patent No. 6673895  
; GENERAL INFORMATION:  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 209671US0  
; CURRENT APPLICATION NUMBER: US/09/881,710  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 30



Qy 1 SSDGLWNNOTQL 13  
 : : | : |  
 Db 7 NXNGSWHXXNTAL 19

RESULT 27

US-08-014-979-117  
 Sequence 117, Application US/08014979

PATENT NO. 5510240

GENERAL INFORMATION:

APPLICANT: Lam, Kit S. et al.  
 TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of Use Thereof

NUMBER OF SEQUENCES: 121  
 CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/014,979

FILING DATE: 19930208

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7156-041

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9080

TELEFAX: 212 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: peptide

US-08-014-979-117

Query Match 29,3%; Score 29; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 6 WNNN 9  
 Db 1 WNNN 4

RESULT 28

US-08-292-968-43  
 Sequence 43, Application US/08292968

PATENT NO. 5656122

GENERAL INFORMATION:

APPLICANT: READ, Randy J.

APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

APPLICANT: OOMEN, Raymond P.

APPLICANT: LOOSMORE, Sheena

APPLICANT: KURIN, Michel H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

APPLICANT: KLEIN, Michel H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

ADDRESSE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/292,968

FILING DATE: 24-AUG-1993

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/110,947

FILING DATE: 31-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I.

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-388

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-968-43

Query Match 29,3%; Score 29; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;Qy 3 DGLWNN 8  
 Db 2 NGLWNND 7

RESULT 29

US-08-467-974-43  
 Sequence 43, Application US/08467974

PATENT NO. 5965385

GENERAL INFORMATION:

APPLICANT: READ, Randy J.

APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

APPLICANT: OOMEN, Raymond P.

APPLICANT: LOOSMORE, Sheena

APPLICANT: KURIN, Michel H.

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

APPLICANT: ARMSTRONG, Glen D.

APPLICANT: HAZES, Bart

TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,974  
 FILING DATE: 31-MAY-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/467,536  
 FILING DATE: 06-JUN-1995  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 FAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-467-974-43

Query Match 29.3%; Score 29; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Qy 3 DGLWN 8 Db 2 NGLWN 7

RESULT 30  
 US-08-467-536-43  
 Sequence 43, Application US/08467536  
 Patent No. 5977304  
 GENERAL INFORMATION:  
 APPLICANT: READ, Randy J.  
 APPLICANT: STEIN, Penelope E.  
 APPLICANT: COCKLE, Stephen A.  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: LOOSMORE, Sheena  
 APPLICANT: KLEIN, Michel H.  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,976  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg

RESULT 31  
 US-08-467-976-43  
 Sequence 43, Application US/08467976  
 Patent No. 6018022  
 GENERAL INFORMATION:  
 APPLICANT: READ, Randy J.  
 APPLICANT: STEIN, Penelope E.  
 APPLICANT: COCKLE, Stephen A.  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: LOOSMORE, Sheena  
 APPLICANT: KLEIN, Michel H.  
 APPLICANT: ARMSTRONG, Glen D.  
 APPLICANT: HAZES, Bart  
 TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,976  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/292,968  
 FILING DATE: 22-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/251,121  
 FILING DATE: 31-MAY-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,947  
 FILING DATE: 24-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEWART, Michael I.  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 43:  
 LENGTH: 7 amino acids  
 SEQUENCE CHARACTERISTICS:  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 PDB ID: 2 NGLWND  
 RESULT 33  
 Query Match 29.3%; Score 29; DB 3; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Mismatches 0; Indels 0; Gaps 0;  
 Sequence 53 Application US/0956322C  
 Patent No. 669660  
 GENERAL INFORMATION:  
 APPLICANT: EPICTIVE PHARMACEUTICALS, INC.  
 APPLICANT: HIAIT, ANDREW C.  
 APPLICANT: HEIN, MICH B.  
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
 FILE REFERENCE: 068904-0501  
 CURRENT APPLICATION NUMBER: US/09/563,222C  
 CURRENT FILING DATE: 2000-05-02  
 PRIORITY NUMBER: 09/563,222  
 PRIORITY FILING DATE: 2000-05-02  
 PRIORITY FILING DATE: 2001-05-02  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 53  
 LENGTH: 7  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-563-222C-53  
 Query Match 29.3%; Score 29; DB 4; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Mismatches 1; Indels 0; Gaps 0;  
 Matches 4; Conservative 1;  
 APPLICANT: GILWNNN 9  
 APPLICANT: 2 GYMRNS 7  
 APPLICANT: 2 GYMRNS 7  
 RESULT 34  
 US-09-570-921-141  
 ; Sequence 141 Application US/09570921  
 ; Patent No. 645525  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SERBES, PIERRE-FRANCOIS  
 ; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
 ; PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION  
 ; FILE REFERENCE: 106213  
 ; CURRENT APPLICATION NUMBER: US/09/370,921  
 ; CURRENT FILING DATE: 2000-05-15  
 ; PRIORITY NUMBER: PCT/FR98/02447  
 ; PRIOR FILING DATE: 1998-11-17  
 ; PRIOR APPLICATION NUMBER: FR/97/14387  
 ; PRIOR FILING DATE: 1997-11-17  
 ; NUMBER OF SEQ ID NOS: 144  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 141  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-570-921-141  
 Query Match 29.3%; Score 29; DB 4; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.3e+02;  
 Mismatches 1; Indels 0; Gaps 0;  
 Sequence 53 Application US/0956322C  
 Patent No. 669660  
 GENERAL INFORMATION:  
 APPLICANT: EPICTIVE PHARMACEUTICALS, INC.  
 APPLICANT: HIAIT, ANDREW C.  
 APPLICANT: HEIN, MICH B.  
 TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
 FILE REFERENCE: 068904-0501  
 CURRENT APPLICATION NUMBER: US/09/563,222C  
 CURRENT FILING DATE: 2000-05-02  
 PRIORITY NUMBER: 09/563,222  
 PRIORITY FILING DATE: 2000-05-02  
 PRIORITY FILING DATE: 2001-05-02  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 53  
 LENGTH: 7  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-563-222C-53  
 Query Match 29.3%; Score 29; DB 4; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
 Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 1;  
 APPLICANT: GILWNNN 9  
 APPLICANT: 2 GYMRNS 7  
 APPLICANT: 2 GYMRNS 7  
 RESULT 35  
 US-0-012-330-52

GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel

TITLE OF INVENTION: Tissue Remodeling

FILE REFERENCE: BEN-SASSON=7

CURRENT APPLICATION NUMBER: US10/032,330

PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: PCT/US00/32852

PRIOR FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: US 09/161,094

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 52

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: synthetic

S-10-032-330-52

RESULT 36

S-08-190-788A-19

Sequence 19, Application US/08190788A

PATENT NO. 5608035

GENERAL INFORMATION:

APPLICANT: Yanofsky, Stephen D.

APPLICANT: Baldwin, Ronald W.

APPLICANT: Baldwin, David N.

APPLICANT: Jacobs, Jeff W.

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor

NUMBER OF SEQUENCES: 312

CORRESPONDENCE ADDRESS:

ADDRESSEE: Afrymax Technologies N.V.

STREET: 4001 Miranda Avenue

CITY: Palo Alto

STATE: California

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,788A

FILING DATE: 01-FEB-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788A

FILING DATE: 02-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 36,691

REFERENCE/DOCKET NUMBER: 1019.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-190-788A-19

RESULT 37

US-08-383-474B-24

Sequence 24, Application US/08383474B

PATENT NO. 5767234

GENERAL INFORMATION:

APPLICANT: Yanofsky, Stephen D.

APPLICANT: Barrett, Ronald W.

APPLICANT: Baldwin, David N.

APPLICANT: Jacobs, Jeff W.

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor

NUMBER OF SEQUENCES: 314

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend & Townsend LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/383,474B

FILING DATE: 01-FEB-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788A

FILING DATE: 02-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 36,691

REFERENCE/DOCKET NUMBER: 1019.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-383-474B-24

RESULT 38

US-08-465-391A-19

; Sequence 19, Application US/08465391A

Patent No. 5767234

QY 1 SSDGLW 6

Db 3 TDGLW 8

## GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: Yanofsky, Stephen D.

APPLICANT: Baldwin, David

APPLICANT: Jacobs, Jeff W.

APPLICANT: Bovy, Phillip R.

APPLICANT: Leahy, Ellen M.

APPLICANT: Pottorf, Richard S.

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-1 Receptor

NUMBER OF SEQUENCES: 405

TITLE OF INVENTION: Peptides and Compounds That Bind to the

CORRESPONDENCE ADDRESS: IL-1 Receptor

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,391A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/373,474

FILING DATE: 01-FEB-1995

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 578331v1el, Vern

REGISTRATION NUMBER: 32,433

REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-465-391A-19

Query Match 28.3%; Score 28; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 3.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSDGLW 6

Db 3 TDDGLW 8

RESULT 39  
US-08-464-538B-19  
Sequence 19, Application US/08464538B

Patent No. 5661476

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: Yanofsky, Stephen D.

APPLICANT: Baldwin, David

APPLICANT: Jacobs, Jeff W.

APPLICANT: Bovy, Phillip R.

APPLICANT: Leahy, Ellen M.

APPLICANT: Pottorf, Richard S.

TITLE OF INVENTION: Peptides and Compounds That Bind to the

## TITLE OF INVENTION: IL-1 Receptor

NUMBER OF SEQUENCES: 402

CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP

ADDRESSEE: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,538B

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/373,474

FILING DATE: 01-FEB-1995

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788

FILING DATE: 02-FEB-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 16528A-001810

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-464-538B-19

Query Match 28.3%; Score 28; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 3.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SSDGLW 6

Db 3 TDDGLW 8

RESULT 40  
US-08-463-076E-63  
Sequence 63, Application US/08463076E

Patent No. 588006

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: Yanofsky, Stephen D.

APPLICANT: Baldwin, David

APPLICANT: Jacobs, Jeff W.

APPLICANT: Bovy, Phillip R.

APPLICANT: Leahy, Ellen M.

APPLICANT: Pottorf, Richard S.

TITLE OF INVENTION: Peptides and Compounds That Bind to the

NUMBER OF SEQUENCES: 392

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463, 076E  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Snyder, Joseph R.  
REGISTRATION NUMBER: 39,381  
REFERENCE/DOCKET NUMBER: 16528A-001850US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-463-0763-63

Query Match 28.3%; Score 28; DB 2; length 8;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 SSDGLW 6  
Db 3 TDDGLW 8

Search completed: December 30, 2004, 16:32:49  
Job time : 39 secs

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 OM protein - protein search, using sw model  
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Scoring table: BLOSSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 35927711 residues

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Minimum DB seq length: 0  
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 Maximum Match 100%  
 Listing first 150 summaries

Database : Published Applications AA:\*

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19:	/cgn2_6/ptodata/1/pubpaas/US09_NEW_PUB_pep:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	34	34.3	12	16	US-10-649-873-131 Sequence 131, App 1590, App
2	34	34.3	20	14	US-0-221-567A-1690 Sequence 18, App
3	33	33.3	18	14	US-0-418-820-18 Sequence 280, App
4	33	33.3	20	10	US-0-971-879-288 Sequence 276, App
5	33	33.3	20	10	US-0-305-736-276 Sequence 275, App
6	33	33.3	20	10	US-0-918-683-273 Sequence 276, App
7	33	33.3	20	11	US-0-818-683-276 Sequence 288, App
8	33	33.3	20	15	US-0-621-401-288 Sequence 289, App
9	31	31.3	19	14	US-0-102-143-28 Sequence 31498, A
10	31	31.3	20	14	US-10-029-386-31498 Sequence 15, App
11	30	30.3	12	11	US-0-805-290A-15 Sequence 6, App
12	30	30.3	13	14	US-0-212-499-6 Sequence 25, App
13	30	30.3	14	10	US-0-932-613-254 Sequence 25, App

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

87	28	28.3	15	15	US-10-149-135-2029	Sequence 2039, APP	GENERAL INFORMATION:
88	28	28.3	15	15	US-10-149-135-2413	Sequence 2413, APP	APPLICANT: Biokine Therapeutics Ltd.
89	28	28.3	15	15	US-10-149-135-2426	Sequence 2426, APP	APPLICANT: Peled, Amnon
90	28	28.3	15	16	US-10-416-249-558	Sequence 558, APP	APPLICANT: Eisenberg, Orly
91	28	28.3	15	17	US-10-691-155-73	Sequence 73, APP	APPLICANT: Valzel-Ohayon, Dalit
92	28	28.3	16	14	US-10-224-999A-623	Sequence 623, APP	TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
93	28	28.3	16	14	US-10-224-999A-624	Sequence 624, APP	FILE REFERENCE: 26732
94	28	28.3	16	14	US-10-224-999A-625	Sequence 625, APP	CURRENT APPLICATION NUMBER: US/10-149, 873
95	28	28.3	16	14	US-10-224-999A-626	Sequence 626, APP	CURRENT FILING DATE: 2003-08-28
96	28	28.3	16	16	US-10-742-350-46	Sequence 46, APP	NUMBER OF SEQ ID NOS: 157
97	28	28.3	17	14	US-10-224-999A-636	Sequence 636, APP	SOFTWARE: PatentIn version 3.2
98	28	28.3	17	14	US-10-224-999A-637	Sequence 637, APP	SEQ ID NO: 131
99	28	28.3	17	14	US-10-224-999A-638	Sequence 638, APP	LENGTH: 12
100	28	28.3	17	14	US-10-224-999A-639	Sequence 639, APP	TYPE: PRT
101	28	28.3	17	14	US-10-224-999A-640	Sequence 640, APP	ORGANISM: Artificial sequence
102	28	28.3	18	14	US-10-106-598-678	Sequence 678, APP	FEATURE: OTHER INFORMATION: synthetic peptide
103	28	28.3	18	14	US-10-224-999A-650	Sequence 650, APP	US-10-649-873-131
104	28	28.3	18	14	US-10-224-999A-652	Sequence 652, APP	;
105	28	28.3	18	14	US-10-224-999A-653	Sequence 653, APP	;
106	28	28.3	18	14	US-10-224-999A-654	Sequence 654, APP	;
107	28	28.3	18	14	US-10-224-999A-655	Sequence 655, APP	;
108	28	28.3	19	14	US-10-224-999A-665	Sequence 665, APP	;
109	28	28.3	19	14	US-10-224-999A-666	Sequence 666, APP	;
110	28	28.3	19	14	US-10-224-999A-667	Sequence 667, APP	;
111	28	28.3	19	14	US-10-224-999A-668	Sequence 668, APP	;
112	28	28.3	19	14	US-10-224-999A-669	Sequence 669, APP	;
113	28	28.3	19	14	US-10-224-999A-670	Sequence 670, APP	;
114	28	28.3	19	14	US-10-224-999A-671	Sequence 671, APP	;
115	28	28.3	19	14	US-10-224-999A-671	Sequence 671, APP	RESULT 2
116	28	28.3	19	16	US-10-416-249-568	Sequence 568, APP	US-10-225-567A-1690
117	28	28.3	19	16	US-10-416-249-568	Sequence 568, APP	;
118	28	28.3	20	14	US-10-224-999A-681	Sequence 681, APP	Sequence 1690, Application US/10225567A
119	28	28.3	20	14	US-10-224-999A-682	Sequence 682, APP	Publication No. US20030113798A1
120	28	28.3	20	14	US-10-224-999A-683	Sequence 683, APP	GENERAL INFORMATION:
121	28	28.3	20	14	US-10-224-999A-684	Sequence 684, APP	;
122	28	28.3	20	14	US-10-224-999A-685	Sequence 685, APP	APPLICANT: Lifespan Biosciences
123	28	28.3	20	14	US-10-224-999A-686	Sequence 686, APP	APPLICANT: Brown, Joseph P.
124	28	28.3	20	14	US-10-224-999A-687	Sequence 687, APP	APPLICANT: Burner, Glenna C.
125	28	28.3	20	14	US-10-224-999A-688	Sequence 688, APP	APPLICANT: Rough, Christine L.
126	28	28.3	20	16	US-10-311-213-18	Sequence 18, APP	TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
127	27.5	27.8	15	9	US-09-732-357A-10	Sequence 10, APP	FILE REFERENCE: 1920-4-4
128	27.5	27.8	15	9	US-09-732-357A-10	Sequence 10, APP	CURRENT APPLICATION NUMBER: US/10-225, 567A
129	27.5	27.8	15	16	US-10-624-884-10	Sequence 10, APP	CURRENT FILING DATE: 2001-12-19
130	27.5	27.8	20	17	US-10-770-013-341	Sequence 341, APP	PRIOR APPLICATION NUMBER: 60/257, 144
131	27.5	27.8	6	15	US-10-460-512-44	Sequence 414, APP	PRIOR FILING DATE: 2000-12-19
132	27	27.3	8	14	US-10-351-641-1651	Sequence 451, APP	NUMBER OF SEQ ID NOS: 2292
133	27	27.3	8	14	US-10-351-641-1663	Sequence 451, APP	SOFTWARE: PatentIn version 3.1
134	27	27.3	9	10	US-10-351-641-1663	Sequence 463, APP	SEQ ID NO: 1690
135	27	27.3	9	10	US-09-733-451-618	Sequence 461, APP	RESULT 3
136	27	27.3	9	14	US-10-283-722-41	Sequence 411, APP	SEQUENCE: Sequence 18, Application US/10418820
137	27	27.3	9	14	US-10-283-722-618	Sequence 418, APP	SEQUENCE: Sequence 18, Application US/10418820
138	27	27.3	9	14	US-10-283-903-41	Sequence 411, APP	SEQUENCE: Sequence 18, Application US/10418820
139	27	27.3	9	14	US-10-283-903-618	Sequence 618, APP	SEQUENCE: Sequence 18, Application US/10418820
140	27	27.3	10	14	US-10-271-343-42	Sequence 42, APP	SEQUENCE: Sequence 18, Application US/10418820
141	27	27.3	10	14	US-10-271-343-43	Sequence 43, APP	SEQUENCE: Sequence 18, Application US/10418820
142	27	27.3	10	14	US-10-271-343-46	Sequence 44, APP	SEQUENCE: Sequence 18, Application US/10418820
143	27	27.3	10	15	US-10-462-462-623	Sequence 623, APP	SEQUENCE: Sequence 18, Application US/10418820
144	27	27.3	10	15	US-10-462-452-636	Sequence 635, APP	SEQUENCE: Sequence 18, Application US/10418820
145	27	27.3	10	15	US-10-462-452-687	Sequence 687, APP	SEQUENCE: Sequence 18, Application US/10418820
146	27	27.3	10	15	US-10-462-452-765	Sequence 765, APP	SEQUENCE: Sequence 18, Application US/10418820
147	27	27.3	10	15	US-10-624-884-10	Sequence 771, APP	SEQUENCE: Sequence 18, Application US/10418820
148	27	27.3	10	15	US-10-609-217-667	Sequence 667, APP	SEQUENCE: Sequence 18, Application US/10418820
149	27	27.3	10	15	US-10-651-723-667	Sequence 667, APP	SEQUENCE: Sequence 18, Application US/10418820
150	27	27.3	10	15	US-10-651-723-667	Sequence 667, APP	SEQUENCE: Sequence 18, Application US/10418820

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; PRINTER APPLICATION NUMBER: 60/374,066
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 18
; ORGANISM: Candida tropicalis
; US-10-418-820-18

Query Match      33.3%; Score 33; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   4 GLWNN 8
Db   1 GLWNN 5

RESULT 4
US-09-974-879-288
; Sequence 288, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/305,736
CURRENt FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: PCT/US98/23435
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 60/064,911
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,912
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,983
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,988
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,987
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,908
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,984
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,985
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066,094
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,100
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,089
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,095
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,090
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 611
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 276
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-879-288

RESULT 5
US-09-305-736-276
; Sequence 276, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
CURRENT APPLICATION NUMBER: US/09/305,736
CURRENt FILING DATE: 1998-05-05
EARLIER APPLICATION NUMBER: PCT/US98/23435
EARLIER FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/064,911
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,900
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,908
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,984
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,983
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/066,089
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,100
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,095
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,090
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 276
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-305-736-276

Query Match      33.3%; Score 33; DB 10; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.e-02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy   5 LWNNTQFLREHS 18
Db   5 LVTNNQTORLQEAE 18

RESULT 6
US-09-818-683-276
; Sequence 276, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins

```



ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC020728\_4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5

US-10-029-386-31498

Query Match

Score 31; DB 14; Length 20;

Best Local Similarity 60.0%; Pred. No. 6.9e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 11  
US-09-805-290A-15

Query Match

Sequence 15, Application US/09805290A

Publication No. US20040002583A1

GENERAL INFORMATION:

APPLICANT: BEZEMER, Sandra

APPLICANT: VAN DER BURG, Monique

APPLICANT: DE HAARD, Johannes J

APPLICANT: TARZILUS, Erwin

TITLE OF INVENTION: USE OF ANTI-BODIES

FILE REFERENCE: F7526-US [V1; PEK/JVT] seq11829Aug2001

CURRENT APPLICATION NUMBER: US/09/805,290A

PRIORITY APPLICATION NUMBER: EP 00200930.6

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 15

LENGTH: 12

TYPE: PRT

ORGANISM: Lama sp.

US-09-805-290A-15

Query Match

Score 30; DB 11; Length 12;

Best Local Similarity 60.5%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 12  
US-0-212-499-6

Query Match

Sequence 6, Application US/10212499

Publication No. US20030135036A1

GENERAL INFORMATION:

APPLICANT: Lanza, Francois

APPLICANT: Phillips, David R.

APPLICANT: Carenave, Jean-Pierre

TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan Lewis &amp; Bockius LLP

STREET: 1800 M St., NW

CITY: Washington

STATE: DC

COUNTRY: US

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/212,499

FILING DATE: 06-Aug-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/560,814

FILING DATE: 2000-04-28

APPLICATION NUMBER: US 08/089,455

FILING DATE: 1993-07-09

APPLICATION NUMBER: US 08/195,006

FILING DATE: 1994-02-10

APPLICATION NUMBER: US 08/884,571

FILING DATE: 1997-06-27

ATTORNEY/AGENT INFORMATION:

NAME: Reid G. Adler

REGISTRATION NUMBER: 30 988

REFERENCE/DOCKET NUMBER: 44481-5018-04-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-467-7000

TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

MOLECULE TYPE: peptide

FEATURE: NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "KS/6 peptide residues 1-13"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-212-499-6

Query Match

Score 30; DB 14; Length 13;

Best Local Similarity 71.4%; Pred. No. 6.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 14  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 15  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 16  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 17  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 18  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 19  
US-09-932-613-254

Query Match

Score 30; DB 10; Length 14;

Best Local Similarity 38.5%; Pred. No. 6.8e+02;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

RESULT 14  
US-09-932-322-254  
; Sequence 254, Application US/09932322  
; Publication No. US20030194743A1  
; GENERAL INFORMATION:  
; APPLICANT: Dyax Corp.  
; APPLICANT: Beltzner, James P.  
; APPLICANT: Porter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Ladner, Robert Charles  
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)  
; FILE REFERENCE: DDX-018.1 PCT; DDX-018.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,322  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 254  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: BLYS binding polypeptide  
US-09-932-322-254  
Query Match 30.3%; Score 30; DB 10; Length 14;  
Best Local Similarity 38.5%; Pred. No. 6.8e+02; Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
Qy 5 WNNNNOTQFLHEH 17  
Db 2 IWDPLIKLWLPFH 14

RESULT 15  
US-10-460-512-25  
Sequence 25, Application US/10460512  
Publication No. US20040038271A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniel E. H. Afar  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Aya Jakobovits  
; APPLICANT: Arthur B. Raitano  
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE  
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
; FILE REFERENCE: 129 20051  
; CURRENT APPLICATION NUMBER: US/10/460,512  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: US/09/638,203  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 6/0148,935  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 25  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-460-512-25

Query Match 30.3%; Score 30; DB 15; Length 14;  
Best Local Similarity 55.6%; Pred. No. 6.8e+02; Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GLWNNNQTO 12  
Db 1 GLWRNGDQQ 9

RESULT 16  
US-10-466-085A-16  
; Sequence 16, Application US/10466085A

RESULT 17  
US-09-881-710-15  
Sequence 15, Application US/09881710  
Publication No. US20020086403A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINS  
; FILE REFERENCE: 2097910SO  
; CURRENT APPLICATION NUMBER: US/09/881,710  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 6/0212,129  
; PRIOR FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 15  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
US-09-881-710-15

Query Match 30.3%; Score 30; DB 9; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNNQ 10  
Db 10 SSEGAWKHAQ 19

RESULT 18  
US-09-891-710-17  
Sequence 17, Application US/09881710  
Publication No. US20020086403A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline

RESULT 19  
US-09-973-021-73  
Sequence 73, Application US/09973025  
Publication No. US20030182706A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P. C.  
STREET: 110 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/973, 025  
FILING DATE: 10-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612, 973  
FILING DATE: 11-Mar-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32, 205  
REFERENCE/DOCKET NUMBER: 1437-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
MOLECULE TOPLOGY: Linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-973-021-82  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 6 WNNNNOTQFL 15  
Db 7 WGENDTDVFL 16  
RESULT 20  
US-09-973-025-82  
Sequence 82, Application US/09973025  
Publication No. US20030182706A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 110 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/612, 973  
FILING DATE: 11-Mar-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32, 205  
REFERENCE/DOCKET NUMBER: 1437-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
MOLECULE TOPLOGY: Linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-973-025-82  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 6 WNNNNOTQFL 15  
Db 7 WGENDTDVFL 16  
RESULT 21  
US-09-839-303-73  
Sequence 73, Application US/09899303  
Publication No. US2003036110A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE-ANGE  
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
PILE REFERENCE: 209671US0  
CURRENT APPLICATION NUMBER: US/09/881, 710  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 60/212, 129  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 17  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Dengue virus  
RESULT 22  
US-09-881-710-17  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 SSDGLWNNNNTOL 13  
Db 10 SSEGAWGHAQ 19  
RESULT 23  
US-09-973-021-73  
Sequence 73, Application US/09973025  
Publication No. US20030182706A1  
GENERAL INFORMATION:  
APPLICANT: MARTEENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 110 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/973, 025  
FILING DATE: 10-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612, 973  
FILING DATE: 11-Mar-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32, 205  
REFERENCE/DOCKET NUMBER: 1437-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
MOLECULE TOPLOGY: Linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-973-021-82  
Query Match  
Score 30; DB 9; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02;

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 110 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/899,303  
 FILING DATE: 06-JUL-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/612,973  
 FILING DATE: 11-MAR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BYRNE, THOMAS E.  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 816-4000  
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

MOLECULE TOPLOGY: linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
 US-09-899-303-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SDGGLMNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 22  
 US-09-899-303-82  
 Sequence 82, Application US/09899303  
 Publication No. US20010036110A1  
 GENERAL INFORMATION:  
 APPLICANT: MAERTENS, GEERT  
 BOSMAN, FONS  
 BOYMANN, GUY  
 DE MARTYNOFF, GUY  
 BUYER, MARIE-ANGE  
 TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
 NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHVE P.C.  
 STREET: 110 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
 CURRENT FILING DATE: 2001-11-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1  
 SEQ ID NO: 73  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Hepatitis C virus  
 US-09-995-808-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SDGGLMNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 23  
 US-09-995-808-73  
 Sequence 73, Application US/09995808  
 Publication No. US20030095980A1  
 GENERAL INFORMATION:  
 APPLICANT: Imrogenetics N.V.  
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
 FILE REFERENCE: 2551-70  
 CURRENT FILING DATE: 2001-11-29  
 CURRENT APPLICATION NUMBER: US/09/995,808  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1  
 SEQ ID NO: 73  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Hepatitis C virus  
 US-09-995-808-73

Query Match 30.3%; Score 30; DB 10; Length 20;  
 Best Local Similarity 38.5%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SDGGLMNNTQQL 13  
 Db 7 NTNGQWHINSTAL 19

RESULT 24  
 US-09-995-808-82  
 Sequence 82, Application US/09995808  
 Publication No. US20030095980A1  
 GENERAL INFORMATION:  
 APPLICANT: Imrogenetics N.V.  
 TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
 FILE REFERENCE: 2551-70  
 CURRENT FILING DATE: 2001-11-29  
 NUMBER OF SEQ ID NOS: 122  
 SOFTWARE: PatentIn 3.1

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; SEQ ID NO: 82
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-860-82

Query Match          30.3%; Score 30; DB 10; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      6 WNNNOTQFL 15
Db      7 WGENDTDVFV 16

RESULT 25
US-09-995-860-73
; Sequence 73, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:
; APPLICANT: Imgenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995, 791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO: 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-73

RESULT 26
US-09-995-860-82
; Sequence 82, Application US/09995860
; Publication No. US20030118603A1
; GENERAL INFORMATION:
; APPLICANT: Imgenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995, 791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO: 82
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-82

RESULT 27
US-09-995-791-73
; Sequence 73, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Imgenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995, 791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO: 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-73

RESULT 28
US-09-995-791-82
; Sequence 82, Application US/09995791
; Publication No. US20030147918A1
; GENERAL INFORMATION:
; APPLICANT: Imgenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-69
; CURRENT APPLICATION NUMBER: US/09/995, 791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO: 82
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; US-09-995-791-82

RESULT 29
US-10-651-165-38
; Sequence 38, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBIS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651, 165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974, 690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; RESULT 27
; US-09-995-791-73

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; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-38

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.9e+02; 4; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; SEQ ID NO: 15
Db      7 WGENUDTDVFV 16

RESULT 30
US-10-651-165-47
; Sequence 47, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
; APPLICANT: DELEVIS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELLS EPITOPE OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-47

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 38.5%; Pred. No. 9.9e+02; 4; Indels 0; Gaps 0;
Matches 5; Conservative 4; Mismatches 4; SEQ ID NO: 13
Db      7 NTNGSWHINSTL 19

RESULT 31
US-10-651-165-56
; Sequence 56, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
; APPLICANT: DELEVIS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPE OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 47
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-56

RESULT 32
US-10-634-895-15
; Sequence 15, Application US/10634895
; Publication No. US20040049016A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGGIER, Marie-Pierre
; APPLICANT: DEBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINS
; FILE REFERENCE: 203671US0
; CURRENT APPLICATION NUMBER: US/10/634,895
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/09/881,710
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dengue virus
US-10-634-895-15

Query Match          30.3%; Score 30; DB 15; Length 20;
Best Local Similarity 50.0%; Pred. No. 9.9e+02; 3; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 3; SEQ ID NO: 19
Db      7 NXNESSWHKXTL 19

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Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 33  
US-10-634-895-17  
; Sequence 17, Application US/10634895  
; Publication No. US20040049016A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 209671US0  
; CURRENT APPLICATION NUMBER: US/10/634,895  
; CURRENT FILING DATE: 2003-08-06  
; PRIORITY APPLICATION NUMBER: US/09/881,710  
; PRIOR FILING DATE: 2001-08-18  
; PRIOR APPLICATION NUMBER: 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 17  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus  
; US-10-634-895-17

Query Match 30.3%; Score 30; DB 15; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 34  
US-10-311-213-22  
; Sequence 22, Application US/10311213  
; Publication No. US20040101862A1  
; GENERAL INFORMATION:  
; APPLICANT: DESPRES, Philippe  
; APPLICANT: COURAGEOT, Marie-Pierre  
; APPLICANT: DEUBEL, Vincent  
; APPLICANT: CATTEAU, Adeline  
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN  
; FILE REFERENCE: 231164US0CT  
; CURRENT APPLICATION NUMBER: US/10/311,213  
; CURRENT FILING DATE: 2002-12-16  
; PRIORITY APPLICATION NUMBER: PCT/IB01/01570  
; PRIOR FILING DATE: 2001-06-18  
; PRIORITY APPLICATION NUMBER: US 60/212,129  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 22  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dengue virus type 4  
; US-10-311-213-22

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNO 10  
Db 10 SSEGAWKHAQ 19

RESULT 35  
US-10-321-798-73  
; Sequence 73, Application US/10321798  
; Publication No. US20040126395A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
; FILE REFERENCE: 2551-93  
; CURRENT APPLICATION NUMBER: US/10/321,798  
; CURRENT FILING DATE: 2002-12-18  
; PRIORITY APPLICATION NUMBER: 60/418,358  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn 3.1  
; SEQ ID NO: 73  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-10-321-798-73

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 38.5%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDGJWNNNQTL 13  
Db 7 NTNGGWHINSTAL 19

RESULT 36  
US-10-321-798-82  
; Sequence 82, Application US/10321798  
; Publication No. US20040126395A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: purified hepatitis C virus envelope proteins for diagnostic and therapeutic use.  
; FILE REFERENCE: 2551-93  
; CURRENT APPLICATION NUMBER: US/10/321,798  
; CURRENT FILING DATE: 2002-12-18  
; PRIORITY APPLICATION NUMBER: 60/418,358  
; PRIOR FILING DATE: 2002-10-16  
; PRIORITY APPLICATION NUMBER: 10/020,510  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn 3.1  
; SEQ ID NO: 82  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; US-10-321-798-82

Query Match 30.3%; Score 30; DB 16; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.9e+02; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNQTOFL 15  
Db 7 WGENDTDVVF 16

RESULT 37  
US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS

```

; FILE REFERENCE: 310098_406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-563-222-53
; US-10-783-950-53
Query Match 29.3%; Score 29; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.5e+06; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GLMANN 9
Db 2 GYWNNS 7
; RESULT 38
; US-10-783-950-53
; Sequence 53, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICTYE PHARMACEUTICALS, INC.
; APPLICANT: HIAVT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US10/783, 950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563, 222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563, 222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-783-950-53
Query Match 29.3%; Score 29; DB 17; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.5e+06; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GLMANN 9
Db 2 GYWNNS 7
; RESULT 39
; US-10-416-249-557
; Sequence 557, Application US/10416249
; Publication No. US20040132121A1
; GENERAL INFORMATION:
; APPLICANT: DaLtrymple, Brian P.
; APPLICANT: Kongsuwan, Kritaya
; APPLICANT: Wijffels, Gene L.
; APPLICANT: Jennings, Philip A.
; APPLICANT: Kemp, Gregory W.
; TITLE OF INVENTION: METHOD OF IDENTIFYING ANTIBACTERIAL COMPOUNDS
; FILE REFERENCE: CULM42_001APC
; CURRENT APPLICATION NUMBER: US/10/416,249
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PCT/AU01/01436
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: AU PR 1320
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: AU PR 2919
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 678
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Listeria innocua
; US-10-416-249-563
Query Match 29.3%; Score 29; DB 16; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+03; Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 3 DGLMANNQQLF 14
Db 4 EGLPDQNQSLF 15
; Search completed: December 30, 2004, 16:43:26
; Job time : 144 secs

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Om protein - protein search, using sw model

Run on: December 30, 2004, 16:22:44 ; Search time 38 Seconds

Total number of hits satisfying chosen parameters: 3886  
 Minimum DB seq length: 0  
 Maximum DB seq length: 20

(without alignments)  
 45.576 Million cell updates/sec

Title: US-10-718-321-1  
 Perfect score: 99  
 Sequence: 1 SDSGLIWNNTQQLPFLHS 18

Scoring table: BLOSUM62  
 Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886  
 Minimum Match 0%  
 Maximum Match 100%  
 Listing first 150 summaries

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

4:

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	31	3	T-cell receptor beta
2	30	30	3	L-lactate dehydrogenase
3	27	27	3	large protein - bovine
4	26	26	2	T-cell receptor beta
5	26	26	3	T-cell receptor delta
6	25	25	3	T-cell receptor beta
7	24	24	2	T-cell receptor beta
8	24	24	2	T-cell receptor alpha
9	24	24	2	T-cell receptor beta
10	24	24	2	subtilisin (EC 3.4.24.12)
11	24	24	2	lysophospholipase
12	23.5	23	2	S-adenosyl-L-methionine
13	23	23	2	gut pentapeptide - variant
14	23	23	2	surface glycoprotein
15	23	23	2	acetylcholinesterase
16	23	23	2	Ig heavy chain DJ
17	23	23	2	proboscipedia - fly
18	23	23	2	T-cell receptor beta
19	23	23	2	anantin - frogtoxin
20	23	23	2	progesterone receptor
21	23	23	2	L-2,4-diaminobutyryl
22	23	23	2	pyrrolidine-5-carboxylic acid
23	23	23	2	link protein - rat
24	22	22	2	T-cell receptor beta
25	22	22	2	T-cell receptor beta
26	22	22	2	T-cell receptor beta
27	22	22	2	thrombospondin 2
28	22	22	2	T-cell receptor beta
29	22	22	2	T-cell receptor beta

103 18 18.2 9 2 D28854  
 104 18 18.2 9 2 PT0238  
 105 18 18.2 9 2 PT0272  
 106 18 18.2 10 2 PC0753  
 107 18 18.2 11 2 PH0914  
 108 18 18.2 11 2 S04875  
 109 18 18.2 12 2 A29169  
 110 18 18.2 12 2 S68271  
 111 18 18.2 12 2 PT0216  
 112 18 18.2 12 2 S28215  
 113 18 18.2 12 2 A49637  
 114 18 18.2 13 2 S47358  
 115 18 18.2 14 2 PT0077  
 116 18 18.2 14 2 S1766  
 117 18 18.2 14 2 PR0007  
 118 18 18.2 15 1 SFR7  
 119 18 18.2 15 2 I46512  
 120 18 18.2 15 2 PH1366  
 121 18 18.2 15 2 PH0782  
 122 18 18.2 16 2 A46236  
 123 18 18.2 17 2 I46511  
 124 18 18.2 17 2 E53113  
 125 18 18.2 17 2 B61491  
 126 18 18.2 17 2 B31435  
 127 18 18.2 17 2 C84063  
 128 18 18.2 17 2 I76573  
 129 18 18.2 18 2 B48839  
 130 18 18.2 18 2 H64711  
 131 18 18.2 18 2 I50389  
 132 18 18.2 18 2 I54078  
 133 18 18.2 19 2 P0548  
 134 18 18.2 19 2 S74087  
 135 18 18.2 19 2 I39327  
 136 18 18.2 20 2 PN0115  
 137 18 18.2 20 2 S32502  
 138 18 18.2 20 2 PH1326  
 139 18 18.2 20 2 S66222  
 140 18 18.2 20 2 B49493  
 141 18 18.2 20 2 S28435  
 142 18 18.2 20 2 S03987  
 143 18 18.2 20 2 B61497  
 144 17 17.2 6 2 PT0519  
 145 17 17.2 7 2 PT0688  
 146 17 17.2 8 2 PT0724  
 147 17 17.2 8 2 XGHUEU  
 148 17 17.2 9 2 C24180  
 149 17 17.2 9 2 A25199  
 150 17 17.2 10 2 S71868

## ALIGNMENTS

**RESULT 1**  
 F49039  
 T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
 C;Accession: F49039  
 R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
 Eur. J. Immunol. 22, 541-549, 1992  
 A;Title: Variation in T cell receptor V beta and J beta repertoire: analysis using  
 A;Reference: Variance number: A49039; MUID:92164737; PMID:1311263  
 A;Accession: F49039  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-16 <ROS>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:90718)

Query Match 31.3%; Score 31; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 86; Indels 5; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 C;Keywords: T-cell receptor

1 SSDGLNNNQNTQLP 14  
 QY | :| | | |  
 2 SASGPDNSNQPQHF 15

## RESULT 2

I49422  
 L-lactate dehydrogenase (EC 1.1.1.27) chain X - western wild mouse (fragment)  
 N;Alternate names: lactate dehydrogenase C  
 C;Species: Mus spretus (western wild mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I49422  
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
 Mamm. Genome 5, 349-355, 1994  
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A;Reference number: I48934; MUID:94319082; PMID:8043949  
 A;Accession: I49422  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-19 <RES>  
 A;Cross-references: UNIPROT:Q62845; EMBL:U05739; NID:9497076; PIDN:AAB60478.1; PID:94970  
 C;Superfamily: L-lactate dehydrogenase  
 C;Keywords: oxidoreductase

## C;Genetics:

## QY

1 SSDGLNNNQNTQLP 14

| :| | | |

12

Query Match 30.3%; Score 30; DB 2; Length 19;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 1;

## Db

6 SADTAWN 12

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## Db

2 DTLHENSTNLIDS 17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

## QY

3 DGLWNNNQNTQLP 18

| :| | | |

17

Query Match 27.3%; Score 27; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No.

A;Residues: 1-16 <CAS>  
A;Cross-references: EMBL:X60840; NID:950116; PIDN:CAA43233.1; PID:950117  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 26.3%; Score 26; DB 2; Length 16;  
Best Local Similarity 71.4%; Pred. No. 5.4e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NNGQIQLF 14  
Db 9 NNGQIQLF 15

RESULT 5

I46654  
T-cell receptor delta-chain J-delta-3 - pig (fragment)  
C;Species: Sus scrofa domesticus (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Nov-1999  
C;Accession: I46654  
R;Yan, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takigaki, Y.  
J. Immunol. 155, 1981-1993, 1995  
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old  
A;Reference number: I46654  
A;Accession: I46654  
MUID:9536165; PMID:7636249  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-19 <YAN>  
A;Cross-references: GB:D49562; NID:91041176; PIDN:BA08506.1; PID:91041177  
C;Keywords: T-cell receptor

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 35.3%; Pred. No. 6.5e+02; Mismatches 2; Indels 6; Gaps 1;  
Matches 6; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

Qy 6 WNNNQ-----TQTLF 16  
Db 2 WDTRQMYFGAGTKLFV 18

RESULT 6

PH0138  
T-cell receptor beta chain V-D-J region C8 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
C;Accession: PH0138  
R;Martin, R.; Howell, M.D.; Jaraguameda, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Ig  
J. Exp. Med. 173, 19-24, 1991  
A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context  
A;Reference number: PH0135; MUID:91086843; PMID:1702137  
A;Accession: PH0138  
A;Molecule type: mRNA  
A;Residues: 1-13 <MAR>  
C;Keywords: T-cell receptor

Query Match 26.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 WNNNQ 10  
Db 7 WTNNB 11

RESULT 7

PT0589  
T-cell receptor beta chain V-D-J region (141-1A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0589  
R;Reehey, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

Query Match 24.2%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.9e+02; Mismatches 3; Indels 4; Gaps 1;  
Matches 7; Conservative 0; Mismatches 3; Indels 4; Gaps 1;

Qy 1 SSGGLWNNNQIQLF 14  
Db 3 SGDQ---NOAPLF 12

RESULT 10

PC1299  
subtilisin (EC 3.4.21.62) GX - Bacillus sp. (strain 6644) (Fragment)

C;Species: *Bacillus* sp.  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: PCl299  
R;Durham, D.R.  
Bloch. Biophys. Res. Commun. 194, 1365-1370, 1993  
A;Title: The elastolytic properties of subtilisin GX from alkalophilic *Bacillus* sp. strain  
A;Reference number: PCl299; MUID:93356814; PMID:8352796  
A;Accession: PC1299  
A;Molecule type: protein  
A;Residues: 1-16 <DUR>  
A;Cross-references: UNIPROT:Q9R557  
C;Keywords: hydrolase; serine protease

Query Match Similarity 24.2%; Score 24; DB 2; Length 16;

Best local Similarity 42.9%; Pred. No. 1.1e+03; Mismatches 3; Conservative 3; Indels 0; Gaps 0;

Qy 6 WNNNOTQ 12  
| : | : |  
Db 5 WGDNRVQ 11

RESULT 11

S27351  
lysozyme - human  
C;Species: *Homo sapiens* (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S27351  
R;Garrett, D.; Holtberg, F.; Steiner, M.R.; Egan, R.W.; Clark, M.A.

Biochem. J. 288, 831-837, 1992  
A;Title: Butyric acid-induced differentiation of HL-60 cells increases the expression of

A;Reference number: S27350; MUID:93111958; PMID:1471998

A;Accession: S27351  
A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-20 <GKR>

A;Cross-references: UNIPROT:P56643

Query Match Similarity 24.2%; Score 24; DB 2; Length 20;

Best local Similarity 35.7%; Pred. No. 1.4e+03; Mismatches 5; Conservative 3; Indels 0; Gaps 0;

Qy 1 SSDGLWNNNOTQLF 14  
| : | : | : |  
Db 2 ASISLYNSNTISYF 15

RESULT 12

S38763  
S-adenosyl-L-methionine decarboxylase alpha chain - *Acanthamoeba castellani*  
C;Species: *Acanthamoeba castellani*

C;Date: 08-Jun-1994 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004

C;Accession: S38763  
R;Hugo, E.R.; Byers, T.J.

Biochem. J. 295, 203-209, 1993  
A;Title: S-Adenosyl-L-methionine decarboxylase of *Acanthamoeba castellani* (Neff): purif

A;Reference number: S38763; MUID:94029912; PMID:8216217

A;Accession: S38763  
A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-20 <ROG>

A;Cross-references: UNIPROT:P34039

Query Match Similarity 23.7%; Score 23.5; DB 2; Length 20;

Best local Similarity 43.8%; Pred. No. 1.7e+03; Mismatches 7; Conservative 3; Indels 3; Gaps 1;

Qy 1 SDSGLWNNNOTQLFLE 16  
| : | : | : | : |  
Db 2 SSMFVN---TKLILK 14

JH0253

gut pentapeptide - Japanese eel

C;Species: *Anguilla japonica* (Japanese eel)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995

C;Accession: JH0253  
R;Usaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 628-632, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A;Reference number: JH0253; MUID:92062113; PMID:1953755

A;Accession: JH0253  
A;Molecule type: protein

A;Residues: 1-5 <TEES>

A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric junction, and of the circular muscle of the gastro-intestinal junction.

Query Match Similarity 23.2%; Score 23; DB 2; Length 5;

Best local Similarity 25.0%; Pred. No. 2.8e+05; Mismatches 0; Conservative 3; Indels 0; Gaps 0;

Qy 4 GLWN 7  
| : |  
Db 1 GFVN 4

RESULT 14

C61512  
variant surface glycoprotein M1at 1.4 - *Trypanosoma brucei* (fragment)

C;Species: *Trypanosoma brucei* (fragment)  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004

C;Accession: C61512  
R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981  
A;Title: Glycopeptides from variant surface glycoproteins of *Trypanosoma brucei*. C-terminal

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: C61512  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <ROL>

A;Cross-references: UNIPROT:Q7MBSS3

C;Keywords: glycoprotein

Query Match Similarity 23.2%; Score 23; DB 2; Length 8;

Best local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Conservative 3; Indels 0; Gaps 0;

Qy 6 WNNN 9  
| : |  
Db 1 WENN 4

RESULT 15

A41117  
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)

C;Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)

C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004

C;Accession: A41117  
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Havikaar, A.; Hucho, F.

Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torpedo* ar

A;Reference number: A41117; MUID:91296772; PMID:2068091

A;Accession: A41117  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <RKE>

A;Cross-references: UNIPROT:Q7L2Z7

C;Keywords: carboxylic ester hydrolase

Query Match Similarity 23.2%; Score 23; DB 2; Length 8;

Best local Similarity 60.0%; Pred. No. 2.8e+05; Mismatches 3; Conservative 1; Indels 0; Gaps 0;

Qy 5 LWNN 9

RESULT 13

Db : |||  
Db : 4 MNPN 8

RESULT 16  
 Ig heavy chain DJ region (clone C100-91A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1344  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 175, 157-181, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1344  
 A;Molecule type: DNA  
 A;Residues: 1-10 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 23.2%; Score 23; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 9.6e-02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 1; Del 0; Insert 0;

Qy 2 SDGLW 6  
 Db 2 SDGDN 6

RESULT 17  
 proboscipedia - fruit fly (*Drosophila pseudoobscura*) (fragment)  
 C;Species: *Drosophila pseudoobscura*  
 C;Accession: A44874  
 R;Randazzo, F.M.; Cribbs, D.L.; Kaufman, T.C.  
 Development 113, 257-271, 1991  
 A;Title: Rescue and regulation of *proboscipedia*: a homeotic gene of the Antennapedia Complex  
 A;Reference number: A44874; MUID:92111389; PMID:1684932  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Accession: A44874  
 A;Note: sequence extracted from NCBI backbone (NCBIN:77929, NCBI:77931)  
 C;Genetic DB: FlyBase:Dpsa/pb  
 A;Cross-references: Flybase:FBgn0012734  
 C;Superfamily: unassigned homeobox proteins; homeobox homology  
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 23.2%; Score 23; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.7e-03; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 1; Del 0; Insert 0;

Qy 6 WNNN 9  
 Db 5 WGNN 8

RESULT 18  
 T-cell receptor beta-chain joining region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999  
 C;Accession: S51735  
 R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.  
 submitted to the EMBL Data Library, November 1993  
 A;Reference number: S51732  
 A;Accession: S51735  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <DUR>  
 A;Cross-references: EMBL:228344; NID:g607122; PID:CA082198.1; PID:g607123

Query Match 23.2%; Score 23; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 4; Del 0; Insert 0;

Qy 1 SSDGLWNQQ 10  
 Db 4 SSDRIGNQPO 13

RESULT 19  
 A61211  
 ananitin - *Streptomyces coeruleescens*  
 C;Species: *Streptomyces coeruleescens*  
 C;Date: 03-May-1994 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C;Accession: A61211  
 R;Wiers, D.F.; Lahm, H.W.; Maeneberg, M.; Labhardt, A.M.  
 J. Antibiot. 44, 172-180, 1991  
 A;Title: Ananitin -- a peptide antagonist of the atrial natriuretic factor (ANF). II. Determination of the structure  
 A;Reference number: A61211; MUID:9185186; PMID:1826288  
 A;Accession: A61211  
 A;Molecule type: protein  
 A;Residues: 1-17 <WYS>  
 A;Cross-references: UNIPROT:Q7M0J9  
 A;Note: the isopeptide linked residue 8 is shown as Asn rather than Asp  
 P;1-8/Cross-link: isopeptide amino end (Gly-Asn) #status experimental

Query Match 23.2%; Score 23; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.7e-03; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 1; Del 0; Insert 0;

Qy 6 WNNN 9  
 Db 5 WGNN 8

RESULT 20  
 progesterone receptor-related protein p23 - rabbit (fragment)  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Accession: C56211  
 C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Jun-2000  
 R;Johnson, J.L.; Beito, T.G.; Krco, C.J.; Toft, D.O.  
 Mol. Cell. Biol. 14, 1956-1963, 1994  
 A;Title: Characterization of a novel 23-kilodalton protein of inactive progesterone receptor  
 A;Reference number: A56211; MUID:94158868; PMID:8114727  
 A;Accession: C56211  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-18 <OH>  
 C;Superfamily: steroid hormone receptor  
 C;Keywords: steroid hormone receptor

Query Match 23.2%; Score 23; DB 2; Length 18;  
 Best Local Similarity 27.3%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
 Matches 3; Conservative 4; Mismatches 4; Del 0; Insert 0;

Qy 6 WNNNQTQFLIE 16  
 Db 8 WYDRDYVFFIE 18

RESULT 21  
 A44854  
 L-Diaminobutyrate decarboxylase (EC 4.1.1.-) - *Acinetobacter calcoaceticus* (fragment)  
 N;Alternate names: DABA decarboxylase  
 C;Species: *Acinetobacter calcoaceticus*  
 C;Date: 31-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C;Accession: A44854; A41817  
 R;Yamamoto, S.; Iizuka, Y.; Tougo, K.; Shinoda, S.  
 J. Gen. Microbiol. 138, 1461-1465, 1992  
 A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *A.*

A;Reference number: A44854; MUID:92381494; PMID:1512577  
A;Accession: A44854  
A;Molecule type: protein  
A;Residues: 1-19 <YAM>  
A;Cross-references: UNIPROT:Q9R519  
A;Experimental source: ATCC 23055  
A;Note: sequence extracted from NCBI backbone (NCBIP:112331)  
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 23.2%; Score 23; DB 2; Length 19;  
Best Local Similarity 42.9%; Pred. No. 2e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LWNNTQ 11  
Db 11 LWNDAES 17

RESULT 22

S16202  
pyrroline-5-carboxylate reductase - soybean chloroplast  
C;Species: chloroplast Glycine max (soybean)  
C;Accession: S16202  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
R;Chilson, O. P.; Kelly-Chilson, A.E.; Siegel, N.R.  
Arch. Biochem. Biophys. 288, 357, 1991  
A;Title: Pyrroline-5-carboxylate reductase in soybean nodules: isolation/partial primary  
A;Reference number: S16202; MUID:91378472; PMID:1898034  
A;Accession: S16202  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <ARC>  
C;Genetics:  
A;Genome: chloroplast  
C;Keywords: chloroplast

Query Match 23.2%; Score 23; DB 2; Length 20;  
Best Local Similarity 30.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 SDGLWNNTQ 11  
Db 7 AEGQWRRDVT 16

RESULT 23

S55756  
link protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Accession: S55756  
C;Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
R;Rhodes, C.; Yamada, Y.  
Nucleic Acids Res. 23, 2305-2313, 1995  
A;Title: Characterization of a glucocorticoid responsive element and identification of a  
A;Reference number: S55756; MUID:95334387; PMID:7610060  
A;Accession: S55756  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-20 <RHO>  
A;Cross-references: EMBL:X5507  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991

Query Match 23.2%; Score 23; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WNNNQ 10  
Db 16 WNSGQ 20

RESULT 24

PH0923

T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C;Accession: PH0923  
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A;Reference number: PH0891; MUID:92078857; PMID:183012  
A;Accession: PH0923  
A;Molecule type: mRNA  
A;Residues: 1-10 <GOL>  
A;Experimental source: concanavalin A-activated lymphoblast  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 22; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WNNNQ 10  
Db 4 WGRNQ 8

RESULT 25

PH1471  
T-cell receptor beta chain (clone A24/PEF4) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Accession: PH1471  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pammenter, C.; Regnault, A.; Koz  
J. Exp. Med. 177, 811-820, 1993  
A;Title: T cell receptor selection by and recognition of two class I major histocompatibility  
A;Reference number: PH1430; MUID:93171821; PMID:8436911  
A;Accession: PH1471  
A;Molecule type: mRNA  
A;Residues: 1-14 <CAS>  
A;Experimental source: cytolytic T-lymphocyte  
C;Keywords: receptor; T-cell

Query Match 22.2%; Score 22; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NNNGTQLP 14  
Db 6 DNQDTQYF 13

RESULT 26

G49655  
T cell-receptor beta chain variable region (clone 1) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Accession: G49655; RA9555; K46655  
C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C;Accession: G49655; RA9555; K46655  
R;Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, B.; Glass, D.N.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993  
A;Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juvenile  
A;Reference number: A49655; MUID:94068553; PMID:8248215  
A;Accession: G49655  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-15 <GR1>  
A;Experimental source: hip joint, synovial tissues  
A;Note: this was designated clone 1  
A;Note: sequence extracted from NCBI backbone (NCBIP:140453)  
A;Accession: F49655  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-15 <GR2>  
A;Experimental source: hip joint, synovial tissues  
A;Note: sequence extracted from NCBI backbone (NCBIP:140451)  
A;Note: this was designated clone 2  
A;Accession: A49655

A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-15 <GRO>  
 A;Experimental source: knee joint, synovial fluid lymphocytes  
 A;Note: this was designated clone SF-1  
 A;Reference: sequence extracted from NCB1 backbone (NCBIP:140445)  
 C;Keywords: T-cell receptor

Query Match 22.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 2.2e+03; Mismatches 5; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 SSDGLIWNNOQ 10  
 Db 5 SPDAGWTDQ 14

RESULT 27

B45474 thrombospondin 2 - bovine (fragment)

N;Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog

C;Species: Bos primigenius taurus (cattle) #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: B45474 R;Pellerin, S.; Lafeuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Feil J. Biol. Chem. 268, 4304-4310, 1993

A;Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by adr

A;Reference number: A45474; MUID:93179438; PMID:8382699

A;Accession: B45474 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <PEL>

A;Cross-references: UNIPROT:09TS97  
 A;Experimental source: adrenocortical cells (NCBIP:125842)

A;Note: sequence extracted from NCB1 backbone (NCBIP:125842)

Query Match 22.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+03; Mismatches 1; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NQNTQ 12  
 Db 2 NNOAQ 6

RESULT 28 S57519

T cell receptor beta chain V region - human (fragment)

C;Species: Homo sapiens (man) #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999

C;Accession: S57519 R;Burrows, S.R.; Sliney, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaez, V.P.

Submitted to the EMBL Data Library, June 1995 A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A;Reference number: S57519 A;Accession: S57519 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Cross-references: EMBL:Z49926; PIDN:9887498; PIDN:CAA90172.1; PID:9887499

C;Keywords: T-cell receptor

Query Match 22.2%; Score 22; DB 2; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+03; Mismatches 3; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SSDGLIWNNOQLF 14  
 Db 3 SSQGLISISSVQYF 16

RESULT 29 S57556

Query Match 22.2%; Score 22; DB 2; Length 19;

C;Keywords: T-cell receptor

RESULT 29

Best Local Similarity 41.7%; Pred. No. 2.8e+03; Mismatches 5; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SSDGLWNNTQ 12  
 Db 8 SLDVENNEWWRK 19

RESULT 32

A;Title: Characterization of a putative 23S rRNA operon of *Buchnera aphidicola* (endosymbiont) - *Buchnera aphidicola* (fragment)  
 A;Accession: I40063  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 C;Species: *Buchnera aphidicola*  
 C;Accession: I40063  
 R;Rouhbakhsh, D.; Baumann, P.  
 Gene 155, 107-112, 1995

A;Reference number: I40061; MUID:5521214; PMID:535281

A;Accession: I40063  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-19 <RES>  
 A;Cross-references: UNIPROT:Q44609; EMBL:U10497; NID:g854713; PIDN:AAA79126.1; PID:g854713; Cross reference: Q44609  
 C;Genetics:  
 A;Gene: aroE  
 C;Keywords: oxidoreductase

Query Match 22.2%; Score 22; DB 2; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LWNN 8  
 Db 4 LWND 7

RESULT 33

R;phycoerythrin gamma-C chain - red alga (*Gastroclonium coulteri*) (fragment)  
 C;Species: *Gastroclonium coulteri*  
 C;Accession: H22565  
 R;Klotz, A.V.; Glaser, A.N.  
 J. Biol. Chem. 260, 4855-4863, 1985  
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A;Reference number: A22565; MUID:85182601; PMID:3886644  
 A;Molecule type: protein  
 A;Residues: 1-20 <KLO>  
 A;Cross-references: UNIPROT:07M270  
 C;Superfamily: Aglaothamnion neglectum R-phycoerythrin gamma chain 33

Query Match 22.2%; Score 22; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 3e+03; Mismatches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MNMQQLP 14  
 Db 8 HHEETQIF 15

RESULT 34

A39308 Glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - *Clostridium sticklandii*  
 C;Species: *Clostridium sticklandii*  
 C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 09-Jul-2004  
 C;Accession: A39308  
 R;Stadtman, T.C.; Davis, J.N.  
 J. Biol. Chem. 266, 22147-22153, 1991  
 A;Title: Glycine reductase protein C. Properties and characterization of its role in the  
 A;Reference number: A39308; MUID:92042141; PMID:1939235  
 A;Accession: A39308  
 A;Status: preliminary

A;Molecule type: protein  
 A;Residues: 1-8 <STA>  
 A;Cross-references: UNIPROT:Q7MM0J  
 C;Function:  
 A;Description: glycine reductase complex catalyzes the reductive deamination of glycine t  
 C;Keywords: ATP; oxidoreductase

RESULT 35

PT0562 T-cell receptor beta chain V-D-J region (126-1AK) - mouse (fragment)  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0562  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-9 <FBE>  
 A;Experimental source: day 18 fetal thymus, strain BALB/C  
 C;Keywords: T-cell receptor

Query Match 21.2%; Score 21; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSDGLW 6  
 Db 2 SSDDNW 7

RESULT 36

PH1308 Ig heavy chain DJ region (clone C731-94) - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1308  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1308  
 A;Molecule type: DNA  
 A;Residues: 1-12 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 21.2%; Score 21; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+03; Mismatches 1; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLWN 7  
 Db 8 GQWN 11

RESULT 37

S57572 T cell receptor V-J junctional alpha chain region - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
 C;Accession: S57572  
 R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argatoff, V.P.

submitted to the EMBL Data Library. June 1995  
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified to

A;Reference number: S57494

A;Accession: S57572

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-14 <BUR>

A;Cross-references: EMBL:249957; NID:9887478; PIDN:CAA90228.1; PID:9887479

C;Keywords: T-cell receptor

Query Match 21.2%; Score 21; DB 2; Length 14;

Best Local Similarity 33.3%; Pred. No. 2.9e+03; Mismatches 3; Conservative 3; Indels 0; Gaps 0;

Matches 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 WNNNOTQFLP 14

Db 5 WSGNTPLVF 13

RESULT 38

PH1994 Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: PH1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 3179, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1594

A;Molecule type: DNA

A;Residues: 1-14 <IEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 21.2%; Score 21; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.9e+03; Mismatches 3; Conservative 0; Indels 0; Gaps 0;

Matches 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GLW 6

Db 11 GLW 13

RESULT 39

A59046 alpha-conotoxin MII - cone shell (Conus magus)

C;Species: Conus magus (magus cone)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: A59046

R;Cartier, G.B.; Yoshikami, D.; Gray, W.R.; Iuo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 752-758, 1996

A;Title: A new alpha-conotoxin which targets alpha<sub>3</sub>beta<sub>2</sub> nicotinic acetylcholine receptor

A;Reference number: A59046; MUID:66205934; PMID:6631783

A;Accession: A59046

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <CAR>

A;Cross-references: UNIPROT:P56636

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin

C;Superfamily: alpha-conotoxin

F;:-16/Product: alpha-conotoxin MII #status experimental <MAT>

F;:-8,3-16/Diulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.2%; Score 21; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 4; Conservative 0; Indels 0; Gaps 0;

Matches 4; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LEHS 18

Db 10 LEHS 13

RESULT 40

S28213 Glutathione transferase (EC 2.5.1.18) - European toad (fragments)

C;Species: Bufo bufo (European toad)

C;Accession: S28213 #sequence\_revision 11-Jun-1999

R;Aceto, A.; Dragani, B.; Buccarelli, T.; Sacchetta, P.; Martini, F.; Angelucci, S.: An

Biochem. J. 289, 417-422, 1993

A;Title: Purification and characterization of the major glutathione transferase from adu-

A;Reference number: S28213; MUID:93143709; PMID:8424786

A;Molecule type: protein

A;Residues: 1-16 <ACB>

A;Experimental source: liver

C;Keywords: transferase

Query Match 21.2%; Score 21; DB 2; Length 16;

Best Local Similarity 45.5%; Pred. No. 3.4e+03; Mismatches 5; Conservative 1; Indels 2; Gaps 1;

Matches 5; Mismatches 3; Indels 2; Gaps 1;

Qy 6 WNNNOTQFLP 16

Db 4 WDNEAN--FLE 12

Search completed: December 30, 2004, 16:32:07

Job time : 40 SECs

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## OM protein - protein search, using SW model

Run on: December 30, 2004, 16:14:44 ; Search time 188 Seconds  
55.089 Million cell updates/sec

Title: US-10-718-321-1

Perfect score: 99

Sequence: 1 SSDGLWNNNQTLFLEHS 18

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 14317

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : UniProt\_02:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
3: uniprot\_pir:  
4: uniprot\_psipred:  
5: uniprot\_swissprot:  
6: uniprot\_ncbi:  
7: uniprot\_ncbiml:  
8: uniprot\_ncbiml2:  
9: uniprot\_ncbiml3:  
10: uniprot\_ncbiml4:  
11: uniprot\_ncbiml5:  
12: uniprot\_ncbiml6:  
13: uniprot\_ncbiml7:  
14: uniprot\_ncbiml8:  
15: uniprot\_ncbiml9:  
16: uniprot\_ncbiml10:  
17: uniprot\_ncbiml11:  
18: uniprot\_ncbiml12:  
19: uniprot\_ncbiml13:  
20: uniprot\_ncbiml14:  
21: uniprot\_ncbiml15:  
22: uniprot\_ncbiml16:  
23: uniprot\_ncbiml17:  
24: uniprot\_ncbiml18:  
25: uniprot\_ncbiml19:  
26: uniprot\_ncbiml20:  
27: uniprot\_ncbiml21:  
28: uniprot\_ncbiml22:  
29: uniprot\_ncbiml23:  
30: uniprot\_ncbiml24:  
31: uniprot\_ncbiml25:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	30.3	19	2 062545 062545-mus_spretus
2	27	27.3	20	2 065705 065705-bovine resp
3	27	27.3	20	2 08v686 08v686-bovine resp
4	26	26.3	17	2 078378 078378-human immun
5	26	26.3	19	2 09ETX8 09ETX8-helicobacte
6	26	26.3	20	2 09SBY5 09SBY5-drosophila
7	26	26.3	20	2 ARB4726 ARB4726-drosophil
8	25	25.3	10	2 Q9TR47 Q9TR47-bos_tauris
9	25	25.3	19	2 05610 05610-homo_sapien
10	25	25.3	19	2 09BTX7 09BTX7-helicobacte
11	25	25.3	19	2 084197 084197-human respi
12	25	25.3	19	2 091329 091329-human immun
13	25	25.3	19	2 09WJBL 09WJBL-human immun
14	25	25.3	20	1 A0BG_EQUAS A0BG_EQUAS-equin
15	25	25.3	20	2 Q9URC7 Q9URC7-baccharomy
16	24.5	24.7	20	2 Q9R987 Q9R987-nitrosospir
17	24.5	24.7	20	2 Q9R9A5 Q9R9A5-nitrosospir
18	24	24.2	11	2 Q9YEBB Q9YEBB-streptococc
19	24	24.2	11	2 AA060518 AA060518-streptoco
20	24	24.2	11	2 AA060520 AA060520-streptoco
21	24	24.2	11	2 AA060522 AA060522-streptoco
22	24	24.2	11	2 AA060524 AA060524-streptoco
23	24	24.2	11	2 AA060526 AA060526-streptoco
24	24	24.2	11	2 AA060528 AA060528-streptoco
25	24	24.2	11	2 AA060530 AA060530-streptoco
26	24	24.2	13	2 Q7TMB4 Q7TMB4-mus_musculu
27	24	24.2	16	2 Q9R557 Q9R557-bacillus_sp
28	24	24.2	16	2 Q66737 Q66737-equine_infe
29	24	24.2	17	2 Q8IVK5 Q8IVK5-homo_sapien
30	24	24.2	17	2 Q78381 Q78381-human_immun
31	24	24.2	18	2 Q9HBD6 Q9HBD6-homo_sapien

105	21	21.2	14	2	06Q704	Q69704	physocarpus	DR HSSP; P00342; 2LDM.
106	21	21.2	14	2	06Q706	Q69706	physocarpus	FT NON_TER 1
107	21	21.2	14	2	06Q709	Q69709	physocarpus	SEQUENCE 19 AA; 2203 MW;
108	21	21.2	14	2	06Q710	Q69710	physocarpus	80D6B2E6F765516B CRC64;
109	21	21.2	14	2	06Q712	Q69712	physocarpus	Query Match 30.3%; Score 30;
110	21	21.2	14	2	06Q713	Q69713	vauquelina	DB 2; Length 19;
111	21	21.2	14	2	06Q714	Q69714	lynothamnu	Best Local Similarity 71.4%;
112	21	21.2	14	2	AAS65671	Aas65671	lynothamnu	Score 30; Pred. 9.9e+02;
113	21	21.2	14	2	AAS65672	Aas65672	vauquelina	Mismatches 1; Indels 0;
114	21	21.2	14	2	AAS65673	Aas65673	physocarp	Gaps 0;
115	21	21.2	14	2	AAS65674	Aas65674	physocarp	Db 6 SAU1LN 12
116	21	21.2	14	2	AAS65675	Aas65675	physocarp	
117	21	21.2	14	2	AAS65676	Aas65676	physocarp	
118	21	21.2	14	2	AAS65677	Aas65677	physocarp	
119	21	21.2	14	2	AAS65678	Aas65678	physocarp	
120	21	21.2	14	2	AAS65679	Aas65679	physocarp	
121	21	21.2	14	2	AAS65680	Aas65680	physocarp	
122	21	21.2	14	2	AAS65681	Aas65681	physocarp	
123	21	21.2	14	2	AAS65682	Aas65682	physocarp	
124	21	21.2	14	2	AAS65683	Aas65683	physocarp	
125	21	21.2	14	2	AAS65684	Aas65684	physocarp	
126	21	21.2	14	2	AAS65685	Aas65685	physocarp	
127	21	21.2	14	2	AAS65686	Aas65686	physocarp	
128	21	21.2	14	2	AAS65687	Aas65687	neillia a	
129	21	21.2	14	2	AAS65688	Aas65688	neillia s	
130	21	21.2	14	2	AAS65689	Aas65689	neillia s	
131	21	21.2	14	2	AAS65690	Aas65690	neillia s	
132	21	21.2	14	2	AAS65691	Aas65691	neillia t	
133	21	21.2	14	2	AAS65692	Aas65692	neillia t	
134	21	21.2	14	2	AAS65693	Aas65693	neillia t	
135	21	21.2	14	2	AAS65694	Aas65694	neillia t	
136	21	21.2	14	2	AAS65695	Aas65695	neillia t	
137	21	21.2	14	2	AAS65696	Aas65696	neillia u	
138	21	21.2	14	2	AAS65697	Aas65697	neillia u	
139	21	21.2	14	2	AAS65698	Aas65698	stephanan	
140	21	21.2	14	2	AAS65699	Aas65699	stephanan	
141	21	21.2	14	2	AAS65700	Aas65700	stephanan	
142	21	21.2	14	2	AAS65701	Aas65701	stephanan	
143	21	21.2	14	2	AAS65702	Aas65702	stephanan	
144	21	21.2	14	2	AAS65703	Aas65703	stephanan	
145	21	21.2	15	2	OTS007	OT8007	neurospora	Query 3 DGLMNNTNQTLFHS 18
146	21	21.2	15	2	06LAG2	O61a92	oryctolagus	Score 27%; DB 2;
147	21	21.2	15	2	CAA77016	Ca877016	mus musculus	Length 20;
148	21	21.2	17	2	062436	O62436	mus musculus	Best Local Similarity 37.5%;
149	21	21.2	17	2	Q9EP50	Q9EP50	unidenifie	Pred. No. 3.1e+03;
150	21	21.2	18	1	TOP1_KLEAE	P46155	klebsiella	Mismatches 7; Indels 0;
<b>RESULT 1 ALIGNMENTS</b>								
Q8V86	ID Q62545	PRELIMINARY;	PRT: 19 AA.	AC Q62545;	DT 01-JUN-1998 (TREMBREL. 06, Created)	AC Q8V86;	PRELIMINARY;	PRT: 20 AA.
	DT 01-JUN-1998 (TREMBREL. 06, Last sequence update)			DT 01-MAR-2002 (TREMBREL. 20, Created)	DT 01-MAR-2002 (TREMBREL. 20, Last sequence update)			
	DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)			DT 01-JUN-2003 (TREMBREL. 24, Last annotation update)	DE RNA-dependent RNA polymerase major subunit (Fragment).			
	DE Lactate dehydrogenase-C (Fragment).			DE RNA-dependent RNA polymerase major subunit (Fragment).	OS Bovine respiratory syncytial virus (strain A5108) (BRSV).			
	OS Mus spretus (Western wild mouse).			OS Viruses: ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.	OC			
	OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			OC NCBI_TaxID=11247;	NCBI_TaxID=11247;			
	OX NCBI_TaxID=10096;			RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.			
	RN [1]			RC STRAIN=SPRET/Ei;	RC STRAIN=A51908;			
	RP SEQUENCE FROM N.A.			RC MEDLINE=9431082; PubMed=8043949;	RC MEDLINE=21580793; PubMed=11724268;			
	RC STRAIN=SPRET/Ei;			RA Ko M.S., Wang X., Holtton J.H., Hagen M.D., Takahashi N., Maezaki Y.,	RA Yunus A.S., Khattar S.K., Collins P.L., Samal S.K.,			
	RX MEDLINE=9431082; PubMed=8043949;			RA Nadeau J.H.;	RT "Rescue of bovine respiratory syncytial virus from cloned cDNA: entire genome sequence of BRSV strain A5108.";			
	RA Nadeau J.H.;			RT Virus Genes 23:157-164 (2001).	RT Virus Genes 23:157-164 (2001).			
	RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";			RT EMBL; AB29554; AAL49413.1; -.	RT EMBL; AB29554; AAL49413.1; -.			
	RL Mam. Genome 5:349-355 (1994).			DR PIR; PQ0300; PQ0300;	DR PIR; PQ0300; PQ0300;			
	DR IEMBL; U05739; AAB60478-1; -.			GO; GO:003968; RNA-directed RNA polymerase.	GO; GO:003968; RNA-directed RNA polymerase.			
	DR PIR; I49422; I49422.			KW NON_TER 20	KW NON_TER 20			
	DR PIR; I49422; I49422.			SEQENCE 20 AA; 2358 MW; 4F13BA094822ED09 CRC64;	SEQENCE 20 AA; 2358 MW; 4F13BA094822ED09 CRC64;			

Query Match 27.3%; Score 27; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 3.1e+03; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 3 DGLWMNNQTOPLHNS 18  
Db 2 DTLIHENSTNWYLDS 17

RESULT 4

073378 PRELIMINARY; PRT; 17 AA.  
AC Q78378; (TREMBrel. 01, Created)  
DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
DE Immunodeficiency virus type 1, viral sample FLIPRS5A (Florida patient  
B), partial env cds, VS region. (Fragment).  
OS Human immunodeficiency virus I.  
OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
OX NCBI\_TaxID:1676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:92271245; PubMed=1589795;  
RA Ou C.-Y., Ciecielski C.A., Myers G., Bandea C.I., Luo C.C.,  
RA Korber B., T.M., Mullins J.I., Schuchterman G., Berkelman R.L.,  
RA Economou A.N., Witte J.J., Satten G.A., Curran J.W.,  
RA Jaffe H.W.; "Molecular epidemiology of HIV transmission in a dental practice.";  
RL Science 256:1165-1171(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang L.Q., Leigh-Brown A.J.; "Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL; MM2123; AAA44931; --."  
DR GO:GO:0019031; Cviral envelope; IEA.  
FT NON\_TER 1  
FT NON\_TER 17 AA; 1723 MW; 34757935D12CA370 CRC64;  
SQ SEQUENCE 17 AA:

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 NNNOTQLF 14  
Db 4 NTNEMETE 11

RESULT 5

Q9ETX8 PRELIMINARY; PRT; 19 AA.  
AC Q9ETX8;  
DT 01-MAR-2001 (TREMBrel. 16, Created)  
DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)  
DE Glutamate racemase (Fragment).  
GN Name=gir;  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Helicobacteraceae; Helicobacter.  
RN [1] NCBI\_TaxID:210;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21117015; PubMed=1179371;  
RA Occhialini A., Marais A., Urdaci M., Sierra R., Munoz N., Covacci A.,  
RA Megraud F.; "Composition and gene expression of the cag pathogenicity island in  
RT Helicobacter pylori strains isolated from gastric carcinoma and  
RT gastritis patients in Costa Rica."; Infect. Immun. 69:1902-1908 (2001).

Query Match 26.3%; Score 26; DB 2; Length 19;  
Best Local Similarity 31.2%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SSDGLWMNNQTOPLE 16  
Db 3 SGDVIWLEKQAKEWLK 18

SEQUENCE 19 AA; 2252 MW; 6FP0977B6A7CE7C5 CRC64;

RESULT 6

Q6SY55 PRELIMINARY; PRT; 20 AA.  
AC Q6SY55;  
DT 05-JUL-2004 (TREMBrel. 27, Created)  
DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
DE Epidermal growth factor receptor (Fragment).  
GN Name=EGFR; ORFNames=CG10079;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukarya; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydriidae; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA098;  
RA Palsson A., Rouse A., Riley-Berger R., Dworkin I., Gibson G.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV46079; AAB84726; 1; --.  
DR GO:GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 20 AA; 2332 MW; E3AC72FBBF98357 CRC64;  
SQ SEQUENCE 20 AA; 2332 MW; E3AC72FBBF98357 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 4.5e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SDGLWMN 9  
Db 11 SRGLWDSS 18

RESULT 7

A0R04726 PRELIMINARY; PRT; 20 AA.  
ID A0R04726  
AC AAB84726;  
DT 02-MAR-2004 (TREMBrel. 27, Created)  
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)  
DE Epidermal growth factor receptor (Fragment).  
GN EGFR OR CG10079.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydriidae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID:7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CA098;  
RA Palsson A., Rouse A., Riley-Berger R., Dworkin I., Gibson G.;  
RT "Nucleotide variation in the EGFR locus of Drosophila melanogaster.";  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV460749; AAH84726.1; -.  
 KW Receptor.  
 FT  
 SQ SEQUENCE 20 AA; 2332 MW; E3AC72F1BB9E357 CRC64;

Query Match Best Local Similarity 26.3%; Score 26; DB 2; Length 20;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SDGLMNN 9  
 Db 11 SGRGLNDSS 18

RESULT 8

Q9TR47 PRELIMINARY; PRT; 10 AA.

ID Q9TR47; PRELIMINARY; PRT; 10 AA.

AC Q9TR47; PRELIMINARY; PRT; 10 AA.

DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DB Amphoterin homolog (Fragment).

OS Bos taurus (Bovine).  
 OC  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 BOVINE; BOV.  
 OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE

RX MEDLINE=9629671; PubMed=7592757;  
 RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,  
 Nagashima M., Lundh E.R., Vijay S., Nitteck D.;  
 RT "The receptor for advanced glycation end products (RAGE) is a cellular  
 binding site for amphoterin. Mediation of neurite outgrowth and co-  
 expression of rage and amphoterin in the developing nervous system.";  
 RL J. Biol. Chem. 270:25752-25761(1995).

SQ SEQUENCE 10 AA; 1163 MW; 28E503453769B1B CRC64;

Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 10;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWMN 8  
 Db 5 MWNN 8

RESULT 9

Q15610 PRELIMINARY; PRT; 19 AA.

ID Q15610; PRELIMINARY; PRT; 19 AA.

AC Q15610; PRELIMINARY; PRT; 19 AA.

DT 01-NOV-1996 (TREMBrel. 01, Created)  
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)

DE Topoisomerase I (Fragment).

GN Name=TOP1;

OS Homo sapiens (Human).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91099302; PubMed=2176592;

RA Kunze N., Klein M., Richter A., Krippers R.;  
 RT "Structural characterisation of the human DNA topoisomerase I gene  
 promoter";  
 RL Bur, J. Biochem. 194:323-330(1990).

DR EMBL; X22601; CAA6834.1; -.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.

SQ SEQUENCE 19 AA; 2236 MW; 47BD36F44FFEEFB CRC64;

Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;  
 Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Query Match Best Local Similarity 25.3%; Score 25; DB 2; Length 19;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SSDGJWNNTQQLP 14  
 Db 2 SGDHLHNDSQLFFF 15

RESULT 10

Q9EX7 PRELIMINARY; PRT; 19 AA.

ID Q9EX7; PRELIMINARY; PRT; 19 AA.

AC Q9EX7; PRELIMINARY; PRT; 19 AA.

DT 01-MAR-2001 (TREMBrel. 16, Created)  
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)

DE Glutamate racemase (Fragment).

GN Name=glr;

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 Helicobacteraceae; Helicobacter.

OX NCBI\_TaxID=210;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CR41, and CR44;  
 RX MEDLINE=2117015; PubMed=11179371;

RA Occhialini A., Marais A., Urdaci M., Sierra R., Munoz N., Covacci A.,  
 Meigras F.,

RT "Composition and gene expression of the cg pathogenicity island in  
 Helicobacter pylori strains isolated from gastric carcinoma and  
 gastritis patients in Costa Rica.";  
 RT Infect. Immun. 69:1903-1908 (2001).

DR EMBL; AF289388; ARGO9846.1; -.  
 DR EMBL; AF289392; AAG09834.1; -.

FT NON\_TER 1 1

SQ SEQUENCE 19 AA; 2238 MW; 6FF0977B72DFB7C5 CRC64;

Query Match Best Local Similarity 31.2%; Score 25; DB 2; Length 19;  
 Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SSDGJWNNTQQLP 16  
 Db 3 SGDVVWLEKQAKEWIK 18

RESULT 11

Q84197 PRELIMINARY; PRT; 19 AA.

ID Q84197; PRELIMINARY; PRT; 19 AA.

AC Q84197; PRELIMINARY; PRT; 19 AA.

DT 01-NOV-1996 (TREMBrel. 01, Created)  
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TREMBrel. 09, Last annotation update)

DE L protein (Fragment).

OS Human respiratory syncytial virus (subgroup B / strain 15537).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus;  
 OC Human respiratory syncytial virus B.

OX NCBI\_TaxID=11251;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8936169; PubMed=3183631;

RA Johnson P.R., Collins P.L.;  
 RT "The A and B subgroups of human respiratory syncytial virus:  
 RT Comparison of intergenic and gene-overlap sequences.",  
 RL J. Gen. Virol. 69:2901-2906 (1988).

DR EMBL; D00397; BA20958.1; -.

NON\_TER 19 19

SQ SEQUENCE 19 AA; 2100 MW; 8277C94820609735 CRC64;

Query Match Best Local Similarity 31.2%; Score 25; DB 2; Length 19;  
 Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy	3 DGLWNNNOTOTFLEHS 18	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
Db	2 DPINGNSANVLTDS 17	
RESULT 12		
ID	091329	PRELIMINARY; PRT; 19 AA.
AC	091329;	
DT	01-NOV-1998 (TREMBLrel. 08, Created)	
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	
DR	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DR	Envelope glycoprotein (Fragment).	
OS	Human immunodeficiency virus 1.	
GN	Namesenv; Retrovirus; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1] Query Match 25.3%; Score 25; DB 2; Length 19; Best Local Similarity 83.3%; Pred. No. 6.1e-03; Indels 0; Gaps 0; Sequence FROM N.A.	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98285741; PubMed=9621043;	
RA	Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L., Safar M., Barre-Sinoussi F., Kazatchkine M.D.; Virus; Human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial transmission. J. Virol. 72:5831-5839(1998).	
DR	EMBL; U87220; AAC2990.J; GO; GO:0019028; C:viral capsid; IEA.	
DR	GO; GO:0019031; C:viral envelope; IEA.	
DR	GO; GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00516; GP120; 1.	
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.	
FT	NON_TER	1
SQ	SEQUENCE : 19 AA; 2294 MW; 3781714A9E073911 CRC64;	
Query Match	25.3%	Score 25;
Best Local Similarity	83.3%	DB 2;
Matches	5	Length 19;
Conservative	0	Indels 0;
Mismatches	1	Gaps 0;
RESULT 14		
ID	ALBG_EQAS	ALBG_EQAS
AC	P39050;	STANDARD;
DT	01-FEB-1995 (Rel. 31, Created)	PRT; 20 AA.
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Alpha-1B-glycoprotein (Alpha-1B glycoprotein) (Postalbumin) (Fragment).	
GN	Name=ALBG;	
OS	Equus asinus (Donkey)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	
OX	NCBI_TaxID=9793;	
RN	[1] Sequence.	
RP	TISSUE=Plasma;	
RX	MEDLINE=91330579; PubMed=1868686;	
RA	Patterson S.D., Bell K., Shaw D.C.;	
RT	"Donkey and horse alpha 1 B-glycoprotein: partial characterization and new alleles." P. Comp. Biochem. Physiol. 98B:523-528 (1991).	
RL	Comp. Biochem. Physiol. 98B:523-528 (1991).	
CC	-!- FUNCTION: Unknown.	
CC	-!- SUBCELLULAR LOCATION: Secreted.	
CC	-!- TISSUE SPECIFICITY: Plasma.	
RT	Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Plasma.	
FT	NON_TER	20
SQ	SEQUENCE : 20 AA; 2197 MW; 65857DFD468EBD9P CRC64;	20
Query Match	25.3%	Score 25;
Best Local Similarity	55.6%	DB 1;
Matches	5	Length 20;
Conservative	0	Indels 0;
Mismatches	4	Gaps 0;
RESULT 13		
ID	Q9WBL1	PRELIMINARY; PRT; 19 AA.
AC	Q9WBL1;	
DT	01-NOV-1999 (TREMBLrel. 12, Created)	
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Envelope glycoprotein (Fragment).	
GN	Name=env;	
OS	Human immunodeficiency virus 1.	
OC	Viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1] Sequence FROM N.A.	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98285741; PubMed=9621043;	
RA	Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L., Safar M., Barre-Sinoussi F., Kazatchkine M.D.; Virus; Human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial transmission." J. Virol. 72:5831-5839(1998).	
DR	EMBL; U87220; AAC32976.1; GO; GO:0019028; C:viral capsid; IEA.	
DR	GO; GO:0019031; C:viral envelope; IEA.	
DR	GO; GO:0005198; F:structural molecule activity; IEA.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00516; GP120; 1.	
RESULT 15		
ID	Q9URC7	PRELIMINARY; PRT; 20 AA.
AC	Q9URC7;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DB	Lipid-binding protein (Fragment).	
OS	Saccharomyces cerevisiae (Baker's yeast).	
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
OX	NCBI_TaxID=4932;	
RN	[1] Sequence.	
RP		
RX	MEDLINE=91353077; PubMed=1862548;	
RA	Crautz C.E., Snyder S.L., Kambouris N.G.;	
RT	"Calcium-dependent secretory vesicle-binding and lipid-binding proteins of Saccharomyces cerevisiae."	
RL	Yeast 7:229-244 (1991).	
DR	GO; GO:0005853; C:ukaryotic translation elongation factor 1 . . . ; IEA.	
DR	GO; GO:0003746; F:translation elongation factor activity; IEA.	

DR GO: GO:0006414; P:translational elongation; IEA.  
 DR InterPro; IPR001356; EBI BD.  
 DR PFAM; PF00736; EBI\_GNE; I.  
 FT NON\_TER 1 1  
 PT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2388 MW; 594377C8C3E72B0D CRC64;  
 Query Match 25.3%; Score 25; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 6.5e+03;  
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 WNNNOTQ1 13  
 DB 5 WDDDBTNL 12

RESULT 16  
 Q9R97 PRELIMINARY; PRT; 20 AA.  
 ID Q9R97  
 AC Q9R97;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ammonia monooxygenase subunit C1 (Fragment).  
 GN Name=amoC1;  
 OS Nitrosospira sp. Np39-19.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosospira.  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RN STRAIN=NPAV;  
 RX MEDLINE=97306641; PubMed=9163908;  
 RA Klotz M.G., Alzerrreca J., Norton J.M.;  
 RT "A gene encoding a membrane protein exists upstream of the amo genes in ammonia oxidizing bacteria: a third member of the amo operon?";  
 RT FEMS Microbiol. Lett. 150:65-73(1997).  
 RN [4] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RX MEDLINE=21655709; PubMed=11807563;  
 RA Norton J.M., Alzerrreca J.J., Suwa Y., Klotz M.G.;  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 RL Arch. Microbiol. 177:139-149(2002).  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 RN [2] SEQUENCE FROM N.A.  
 RC STRAIN=Np39-19;  
 RA Shiozawa T.L., Norton J.M., Alzerrreca J.J., Klotz M.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 KW Monoxygenase.  
 RL Arch. Microbiol. 177:139-149(2002).  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 RN [2] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RA Norton J.M., Alzerrreca J.J., Suwa Y., Klotz M.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 KW Monoxygenase.  
 RL Arch. Microbiol. 177:139-149(2002).  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 RN [2] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RA Norton J.M., Alzerrreca J.J., Suwa Y., Klotz M.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 KW Monoxygenase.

FT SEQUENCE 20 AA; 2266 MW; A745DC66ACCC3F2A9 CRC64;

Query Match 24.7%; Score 24.5; DB 2; Length 20;  
 Best Local Similarity 31.2%; Pred. No. 7.8e+03;  
 Matches 5; Conservative 6; Mismatches 4; Indels 1; Gaps 1;  
 QY 2 SDGLMNNTQOLFLEH 17  
 DB 2 TDVVW-NGOSKVLNN 16

RESULT 17  
 Q9R9A5 PRELIMINARY; PRT; 20 AA.  
 ID Q9R9A5  
 AC Q9R9A5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ammonia monooxygenase 1 subunit C (Fragment).  
 GN Name=amoC1;  
 OS Nitrosospira sp. Np39-19.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosospira.  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RX MEDLINE=96001263; PubMed=7557469;  
 RA Klotz M.G., Norton J.M.;  
 RT "Sequence of an ammonia monooxygenase subunit A-encoding gene from Nitrosospira sp. NpAV";  
 RT Gene 163:159-160(1995).  
 RN [2] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RX MEDLINE=6275898; PubMed=8674986;  
 RA Norton J.M., Low J.M., Klotz M.G.;  
 RT "The gene encoding ammonia monooxygenase subunit A exists in three nearly identical copies in Nitrosospira sp. NpAV";  
 RT FEMS Microbiol. Lett. 139:181-188(1995).  
 RN [3] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RX MEDLINE=97306641; PubMed=9163908;  
 RA Klotz M.G., Alzerrreca J., Norton J.M.;  
 RT "A gene encoding a membrane protein exists upstream of the amo genes in ammonia oxidizing bacteria: a third member of the amo operon?";  
 RT FEMS Microbiol. Lett. 150:65-73(1997).  
 RN [4] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RX MEDLINE=21655709; PubMed=11807563;  
 RA Norton J.M., Alzerrreca J.J., Suwa Y., Klotz M.G.;  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 RL Arch. Microbiol. 177:139-149(2002).  
 DR EMBL; AR032438; AAC86810.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 KW Monoxygenase.  
 RL Arch. Microbiol. 177:139-149(2002).  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 RN [2] SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;  
 RA Norton J.M., Alzerrreca J.J., Suwa Y., Klotz M.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria";  
 DR EMBL; AR042170; AAC25054.1; -.  
 GO; GO:004497; F:monooxygenase activity; IEA.  
 KW Monoxygenase.

FT SEQUENCE 20 AA; 2266 MW; A745DC66ACCC3F2A9 CRC64;

Query Match 24.7%; Score 24.5; DB 2; Length 20;  
 Best Local Similarity 31.2%; Pred. No. 7.8e+03;  
 Matches 5; Conservative 6; Mismatches 4; Indels 1; Gaps 1;  
 QY 2 SDGLMNNTQOLFLEH 17  
 DB 2 TDVVW-NGOSKVLNN 16

RESULT 18  
 Q5YBB8 PRELIMINARY; PRT; 11 AA.  
 ID Q5YBB8  
 AC Q5YBB8;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Wzx (Fragment).  
 GN Name=wzx;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=MA053392; NSPN001/319, NSPN01/278, MA050663, MA052628, 015009,  
 RC and MA065610;  
 RX MEDLINE=22979121; PubMed=14614062;  
 RA Kong F., Gilbert G.L.;  
 RT "Using cpsA-cpsB sequence polymorphisms and serotype-/group-specific PCR to predict 51 streptococcus pneumoniae capsular serotypes";  
 RT J. Med. Microbiol. 52:1047-1058(2003).  
 RL EMBL; AY163227; AAO60520.1; -.  
 DR EMBL; AY163228; AAO60522.1; -.  
 DR EMBL; AY163229; AAO60524.1; -.  
 DR EMBL; AY163230; AAO60526.1; -.  
 DR EMBL; AY163231; AAO60528.1; -.  
 DR EMBL; AY163232; AAO60530.1; -.  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=NPAV;



Db	1 FLEHT 5	PRELIMINARY;	PRT;	11 AA.
RESULT 23				
AR060526	PRELIMINARY;	PRT;	11 AA.	
AC AA060526				
DT 02-MAR-2004	(TREMBrel. 27, Created)			
DT 02-MAR-2004	(TREMBrel. 27, Last sequence update)			
DT 02-MAR-2004	(TREMBrel. 27, Last annotation update)			
DE WZX (Fragment).				
GN				
OS Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus.				
OX NCBI_TAXID=1313;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=MA050653;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F., Gilbert G.I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:047-058 (2003).				
DR EMBL; AY163230; AA060526.1; -. (2003).				
FT NON_TER 1 1				
SQ SEQUENCE 11 AA; 1456 MW; EE6B29E7C721F1A1 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 11;				
Best Local Similarity 80.0%; Pred. No. 4.8e+03;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 14 FLEHS 18				
Db 1 FLEHT 5				
RESULT 24				
AR060528	PRELIMINARY;	PRT;	11 AA.	
ID AA060528				
AC				
DT 02-MAR-2004 (TREMBrel. 27, Created)				
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)				
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)				
DE WZX (Fragment).				
GN				
OS Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus.				
OX NCBI_TAXID=1313;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=MA050653;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F., Gilbert G.I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:047-058 (2003).				
DR EMBL; AY163231; AA060528.1; -. (2003).				
FT NON_TER 1 1				
SQ SEQUENCE 11 AA; 1456 MW; EE6B29E7C721F1A1 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 11;				
Best Local Similarity 80.0%; Pred. No. 4.8e+03;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY 14 FLEHS 18				
Db 1 FLEHT 5				
RESULT 26				
Q7TM84	PRELIMINARY;	PRT;	13 AA.	
ID Q7TM84				
AC Q7TM84;				
DT 01-OCT-2003 (TREMBrel. 25, Created)				
DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)				
DE UORF4 (UORF2).				
GN Name=ElF5a;				
OS Mus musculus (Mouse).				
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TAXID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=BaLB/c;				
RA Jenkins Z.A., Johansson H.E.;				
RC Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AY129344; AAN17525.1; -.				
DR EMBL; AY129336; AAN17530.1; -.				
DR EMBL; AY129329; AAN17537.1; -.				
DR GO; GO:0005737; Cyttoplasm; IDA.				
DR GO; GO:0005634; Cinnucleus; IDA.				
DR GO; GO:0006915; Papoplosis; IDA.				
SQ SEQUENCE 13 AA; 1477 MW; 8AAH04CCP18E35A5 CRC64;				
Query Match 24.2%; Score 24; DB 2; Length 13;				
Best Local Similarity 50.0%; Pred. No. 5.8e+03;				
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
QY 4 GLMWN 9				
Db 2 GLWSS 7				
RESULT 27				
Q9R557	PRELIMINARY;	PRT;	16 AA.	
ID Q9R557				
AC Q9R557;				
DT 01-MAY-2000 (TREMBrel. 13, Created)				
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)				
RESULT 25				
AA060530				
AC AA060530;				
DT 02-MAR-2004 (TREMBrel. 27, Created)				
DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)				
DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)				
DE WZX (Fragment).				
GN				
OS WZX.				
OC Streptococcus pneumoniae.				
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC Streptococcus.				
OX NCBI_TAXID=1313;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=MA050653;				
RX MEDLINE=22979121; PubMed=14614062;				
RA Kong F., Gilbert G.I.;				
RT "Using cPSA-cPSB sequence polymorphisms and serotype-/group-specific				
RT PCR to predict S1 Streptococcus pneumoniae capsular serotypes.";				
RL J. Med. Microbiol. 52:047-058 (2003).				
DR EMBL; AY163230; AA060530.1; -. (2003).				

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Subtilisin GX (Fragment).  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE:93356814; PubMed=8352796;  
RA Durham D.R.;  
RT "The elastolytic properties of subtilisin GX from alkalophilic  
RT Bacillus sp. strain 6644 provides a means of differentiation from  
RT other subtilisins".  
RL Biochem. Biophys. Res. Commun. 194:1365-1370(1993).  
DR PIR: PC1299; PC1299;  
SQ SEQUENCE 16 AA; 1804 MW; 000FB22F59940C94 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 16;  
Best local Similarity 42.9%; Pred. No. 7.3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 WNNNOTQ 12  
Db 5 WGDNRVO 11

RESULT 28  
ID 066737 PRELIMINARY; PRT; 16 AA.  
AC 066737;  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Transmembrane protein (Fragment).  
OS Equine infectious anemia virus.  
OC Viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wyoming wild type non-cell culture adapted; TISSUE=Blood;  
RX MEDLINE:9229230; PubMed=1318398;  
RA Perry S.T.; Flaherty M.M.; Kelley M.J.; Clabough D.L.; Tronick S.R.,  
RA Coggins L.; Whetter L.; Lenzel C.R.; Fuller F.J.;  
RT "The surface envelope protein gene region of equine infectious anemia  
RT virus is not an important determinant of tropism in vitro.";  
RL J. Virol. 66:4085-4097(1992).  
DR EMBL; M87559; AAA30311;  
DR GO; GO:0005188; F:structural molecule activity; IEA.  
DR GO; GO:0011602; C:integral membrane; IEA.  
DR InterPro; IPR01367; Gp0\_EIAV.  
DR Pfam; PF00971; EIAV\_GP30\_1.  
KW Transmembrane.  
FT NON\_TER 16 16 16 AA;  
SQ SEQUENCE 16 AA; 1918 MW; BAED9AF8B99A3DB4 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 16;  
Best local Similarity 66.7%; Pred. No. 7.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 NNQTOQ 13  
Db 9 NNKITBL 14

RESULT 29  
ID Q8YIK5 PRELIMINARY; PRT; 17 AA.  
AC Q8YIK5;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Steerin2 protein (Fragment).  
GN Name=STEERIN2;

RESULT 30  
ID Q78381 PRELIMINARY; PRT; 17 AA.  
AC Q78381;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DB Immunodeficiency virus type 1, viral sample FLIPRSF (Florida patient  
B), partial env cds, V5 region. (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:92271245; PubMed=1599796;  
RA Ou C.-Y.; Cieslewski C.A.; Myers G.; Bandea C.I.; Luo C.C.,  
RA Korber B.T.M.; Mullins J.I.; Schatzlein G.; Beekelman R.L.,  
RA Economou A.N.; Witte J.J.; Furman L.J.; Satten G.A.; Curran J.W.,  
RA Jaffe H.W.;  
RT "Molecular epidemiology of HIV transmission in a dental practice.";  
RL Science 256:1165-1171(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhang L.Q.; Leigh-Brown A.J.;  
RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; M93126; AAA44961;  
DR GO; GO:0011901; C:viral envelope; IEA.  
DR InterPro; IPR00777; GPI20.  
FT NON\_TER 1  
FT NON\_TER 17 17 17 AA;  
SQ SEQUENCE 17 AA; 1708 MW; 347570D2D12CA370 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 17;  
Best local Similarity 50.0%; Pred. No. 7.8e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 7 NNQTOQF 14  
Db 4 NTNNTETF 11

RESULT 31  
ID Q9HBD6 PRELIMINARY; PRT; 18 AA.  
AC Q9HBD6;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE ATPB (Fragment).  
GN Name=ATPB;  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN NCBI\_TaxID=9606;  
 [1] SEQUENCE FROM N.A.  
 RA Wang N., Wu Z. Y., Murong S.X., Lin M.T., Fang L.;  
 RT "hot point mutations of wilson disease gene in Chinese with DNA  
 sequencing.";  
 RL Chung-Hua Shen Ching Ko Tsa Chih 31:20-23(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Wu Z.Y., Wang N., Murong S.X.;  
 RL Submitted (ABR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AR254565; AAC2752.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2100 MW; B9E7FA2BF70B0B78 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 18;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
 QY 4 GLWNQNOTQFLFLEH 17  
 Db 13 GLW-----LEH 18

RESULT 32

Q9ZG65 PRELIMINARY; PRT; 18 AA.  
 ID Q9ZG65  
 AC Q9ZG65;  
 DT 01-MAY-1999 (TREMBREL\_10, Created)  
 DT 01-MAY-1999 (TREMBREL\_10, Last sequence update)  
 DT 01-MAY-1999 (TREMBREL\_10, Last annotation update)  
 DE Orotidine-5'-phosphate decarboxylase (Fragment).  
 Name=pYRF;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L2 43kB;  
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF008729; AA004068.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2026 MW; CB911767583AF4B3 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 18;  
 Best Local Similarity 36.4%; Pred. No. 8.3e+03;  
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 SDGIGWNNNOT 11  
 Db 2 SSETWSWNTRNS 12

RESULT 33

Q9QHY4 PRELIMINARY; PRT; 19 AA.  
 ID Q9QHY4  
 AC Q9QHY4;  
 DT 01-MAY-2000 (TREMBREL\_13, Created)  
 DT 01-MAY-2000 (TREMBREL\_13, Last sequence update)  
 DT 01-JUN-2000 (TREMBREL\_14, Last annotation update)  
 DE Oligodendrocyte-specific UDP-galactoseceramide galactosyltransferase  
 (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE.

RESULT 34

Q9QV32 PRELIMINARY; PRT; 19 AA.  
 ID Q9QV32  
 AC Q9QV32;  
 DT 01-MAY-2000 (TREMBREL\_13, Created)  
 DT 01-MAY-2000 (TREMBREL\_13, Last sequence update)  
 DT 01-JUN-2002 (TREMBREL\_21, Last annotation update)  
 DE G3.5 ANTI-GEN-ALPHA-actinin (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP Price K.A., Malhotra S.K., Koke J.R.;  
 RA Price K.A., Malhotra S.K., Koke J.R.;  
 RT "Localization and characterization of an intermediate filament-  
 associated protein.";  
 RL Submitted (XKX-1993) to the EMBL/GenBank/DBJ databases.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2205 MW; 505724CB038EB879 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 8.8e+03;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 8 NNQNOTQFLFLEH 17  
 Db 7 NLAMQIFVKH 16

RESULT 35

LPH3\_HUMAN STANDARD; PRT; 20 AA.  
 ID LPH3\_HUMAN  
 AC P56431;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update) (Fragment).  
 DE Lysophospholipase HL-60 peak 3 (EC 3.1.1.5).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leukemia;  
 RX MEDLINE=93111958; PubMed=1471998;  
 RX Garsett D., Hollenberg F., Steiner M.R., Egan R.W., Clark M.A.,  
 RT "Butyric acid-induced differentiation of HL-60 cells increases the  
 expression of a single lysophospholipase.";  
 RL Biochem. J. 288:831-837(1992).  
 CC -I FUNCTION: Degradation of lysophospholipids.  
 CC -I CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =  
 CC glycerophosphocholine + a fatty acid anion.  
 CC -I PTM: The N-terminus is blocked.  
 DR PIR; S27351; S27351.

DR GO; GO:0004622; **P**lyosphospholipase activity; IDA.  
 DR GO; GO:0009395; **P**hospholipid catabolism; NAS.  
 KW Direct protein sequencing; Hydrolase; Lipid degradation.  
 FT NON\_TER 1 1  
 SEQUENCE 20 AA; 2263 MW; 4D298E6D3F21F87F CRC64;  
 Query Match 24.2%; Score 24; DB 1; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 9.3e+03;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 SDSGLWNNTQFLF 14  
 Db 2 ASISLYNSNTISYF 15

RESULT 36  
**OMP\_HAEGA**  
 ID OMP\_HAEGA STANDARD; PRT; 20 AA.  
 AC P8051;  
 DT 10-OCT-2003 (Rel. 42, last sequence update)  
 DT 05-JUL-2004 (Rel. 44, last annotation update)  
 DB Major outer membrane protein (MOMP) (Outer membrane protein H)  
 (Fragment).  
 GN Name=ompH;  
 OS Haemophilus gallinarum.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OX Pasteurellaceae; Haemophilus.  
 NCBI\_TAXID=728;  
 [1] SEQUENCE, AND SUBCELLULAR LOCATION.  
 RC STRAIN=IDPFH 1645 / Serovar A1;  
 RX MEDLINE=96134400; PubMed=8837367;  
 RA Hartmann L., Schroeder W., Luebke-Becker A.;  
 RT "A comparative study of the major outer membrane proteins of the avian  
 Haemophilus and Pasteurella gallinarum.",  
 RL Zentralbl. Bakteriol. 284:47-51 (1996).  
 CC -!- FUNCTION: Structural rigidity of the outer membrane of elementary  
 bodies and porin forming, permitting diffusion of solutes through  
 the intracellular reticular body membrane.  
 CC -!- SUBUNIT: Disulfide bond interactions within and between MOMP  
 molecules and other components form high molecular-weight  
 oligomers.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -!- SIMILARITY: Belongs to the Gram-negative porin family.  
 KW Direct protein sequencing; Outer membrane; Porin; Transmembrane.  
 FT NON\_TER 20  
 SEQUENCE 20 AA; 2142 MW; 2B0C2CED4FEE635CB CRC64;

Query Match 24.2%; Score 24; DB 1; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 37  
**QY950**  
 ID 051950 PRELIMINARY; PRT; 20 AA.  
 AC 051950;  
 DT 01-JUN-1998 (TREMBrel. 05, Created)  
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)  
 DB Major outer membrane protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TAXID=813;  
 RX SEQUENCE FROM N.A.  
 MEDLINE=98055742; PubMed=9395364;

Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 38  
**QY952**  
 ID 051952 PRELIMINARY; PRT; 20 AA.  
 AC 051952;  
 DT 01-JUN-1998 (TREMBrel. 06, Created)  
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)  
 DB Outer membrane protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiaceae; Chlamydia.  
 NCBI\_TAXID=813;  
 RX SEQUENCE FROM N.A.  
 RA Bobo L., Novak N.G.;  
 RT "Severe disease in children with trachoma is associated with  
 persistent Chlamydia trachomatis infection.";  
 RL J. Infect. Dis. 000-0-0 (1998).  
 DR EMBL; AF015550; AAB95378.1; -.  
 FT NON\_TER 1  
 SEQUENCE 20 AA; 2223 MW; D838044775219589 CRC64;  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 9.3e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 39  
**QY951**  
 ID QY951 PRELIMINARY; PRT; 20 AA.  
 AC 077041;  
 DT 01-OCT-2003 (TREMBrel. 25, Created)  
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DB UORF3 (TREMBrel).  
 GN Name=Eliffa;  
 OS Mus musculus (Mouse).  
 OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Jenkins Z.A., Johansson H.E.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY129324; AAC117524; 1; -.  
 DR EMBL; AY129326; AAC117529; 1; -.

DR EMBL; AY129329; AAM17536.1; - .  
 DR GO; GO:000537; C:cytoplasm; IDA.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0006915; P:apoprotein; IDA.  
 SQ SEQUENCE 20 AA; 2265 MW; E3C2BF800E00F3F CRC64;  
  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 3; Mismatches 0;  
  
 QY 4 GLWANN 9 ||||:  
 Db 9 GLWSSS 14

RESULT 40  
 Q90X92 PRELIMINARY; PRT; 20 AA.  
 ID Q90X92; AC 090X92;  
 DT 01-DEC-2001 (TREMBLel. 19, Created)  
 DT 01-DEC-2001 (TREMBLel. 19, Last sequence update)  
 DE Tyrosinase (Fragment).  
 GN Name=TYR.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Deng X., Yang Y., Liu W.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF416915; AAL14561.1; -.  
 FT EMBL 1  
 FT NON-TER 1  
 FT 20 20  
 FT SEQUENCE 20 AA; 2300 MW; AD237P25FAIBA696 CRC64;  
  
 Query Match 24.2%; Score 24; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 9.3e+03; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 3;  
  
 QY 5 DANNNOTL 13 ||||:  
 Db 11 TWANIQSL 19

Search completed: December 30, 2004, 16:31:25  
 Job time : 192 sec